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(19) **United States**(12) **Patent Application Publication**
Carey et al.(10) **Pub. No.: US 2006/0223141 A1**(43) **Pub. Date: Oct. 5, 2006**(54) **TRANSCRIPTION AMPLIFICATION
SYSTEM FOR MOLECULAR IMAGING**(75) Inventors: **Michael F. Carey**, Sherman Oaks, CA
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THE PRESIDENT)**, OAKLAND, CA
(US)(21) Appl. No.: **10/503,642**(22) PCT Filed: **Feb. 7, 2003**(86) PCT No.: **PCT/US03/03847****Related U.S. Application Data**(60) Provisional application No. 60/355,300, filed on Feb.
8, 2002.**Publication Classification**(51) **Int. Cl.****G01N 33/574** (2006.01)**C07H 21/04** (2006.01)**C12P 21/06** (2006.01)**C07K 14/82** (2006.01)**C12N 15/86** (2006.01)(52) **U.S. Cl.** **435/69.1**; 435/456; 435/325;
435/7.23; 530/350; 536/23.5(57) **ABSTRACT**

The present invention provides a transcription amplification system, comprising an effector nucleic acid molecule and a reporter molecule, which work together to produce a heterologous gene product in a cell-type, specific manner. The present invention also relates to methods for producing, detecting, imaging, and monitoring the heterologous gene product in a cell or in a subject.

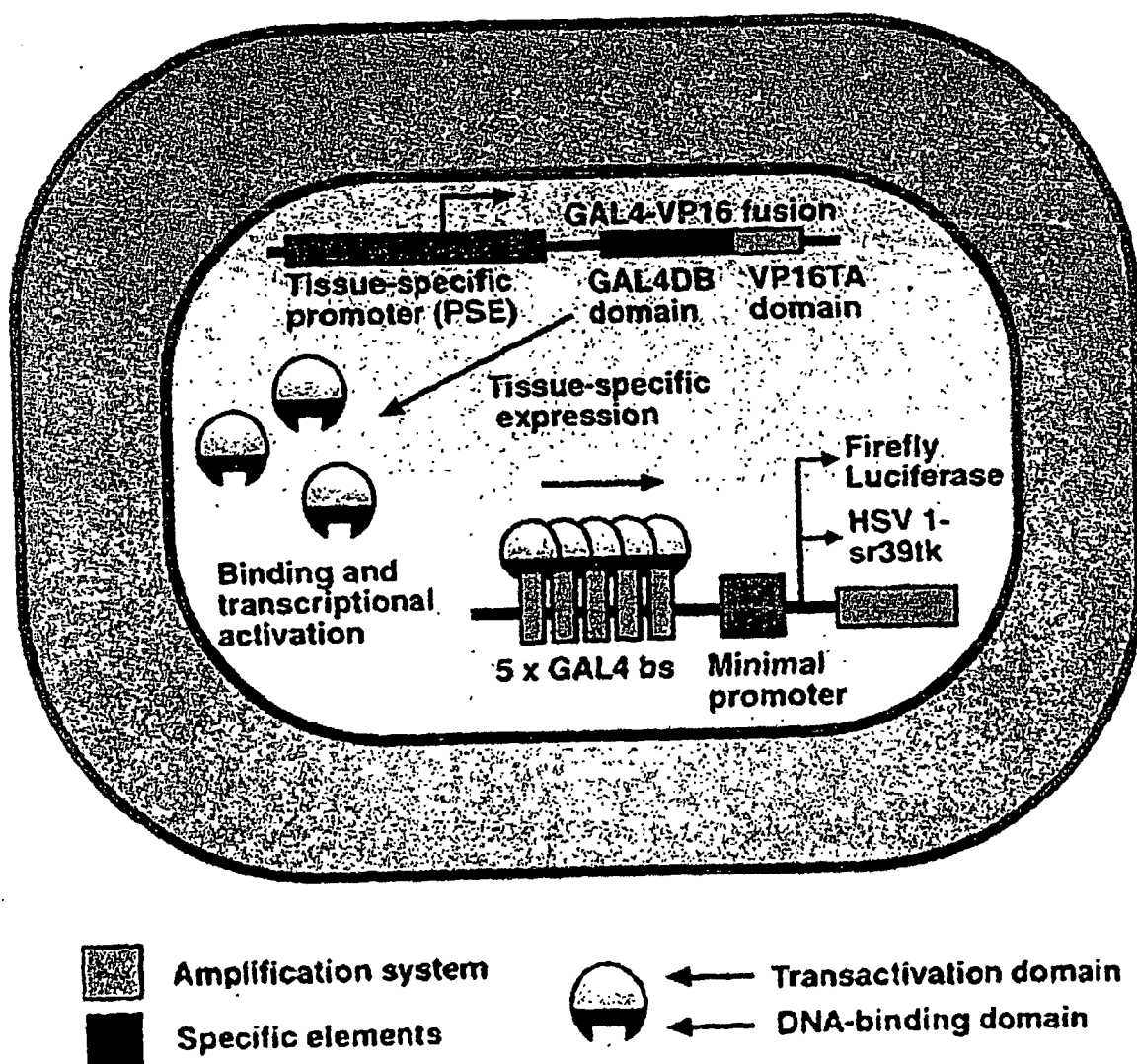


Fig. 1

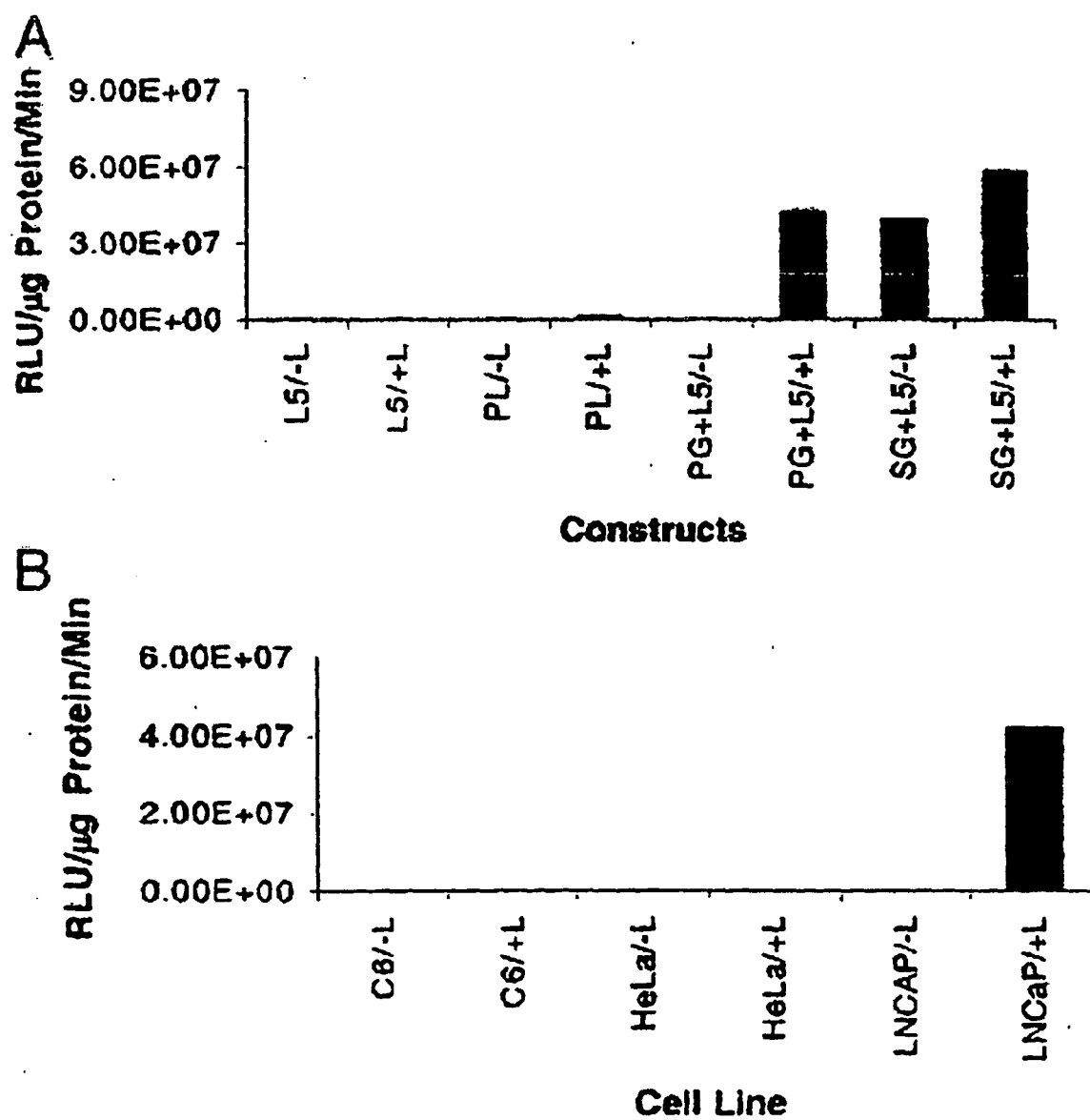


Fig. 2

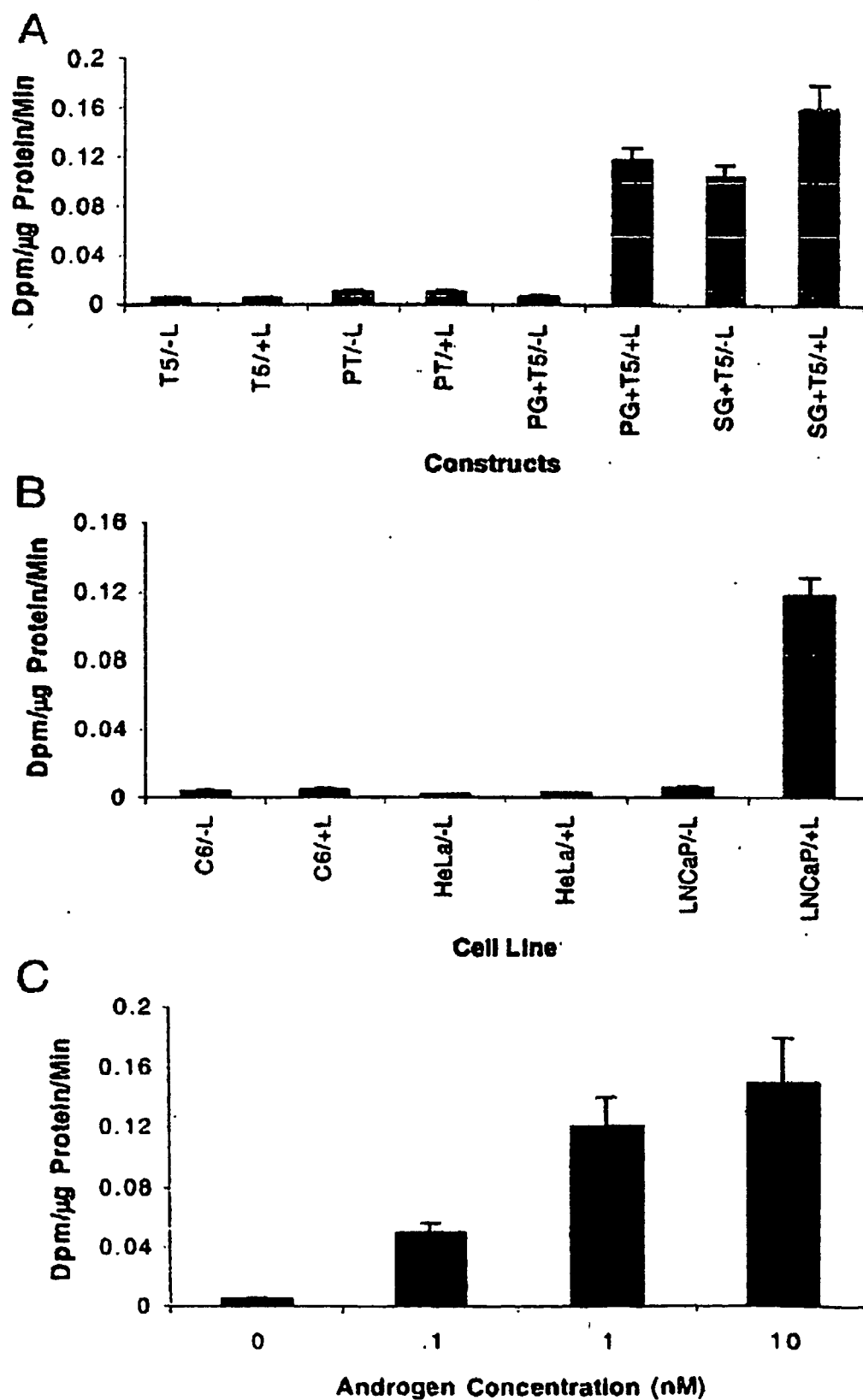
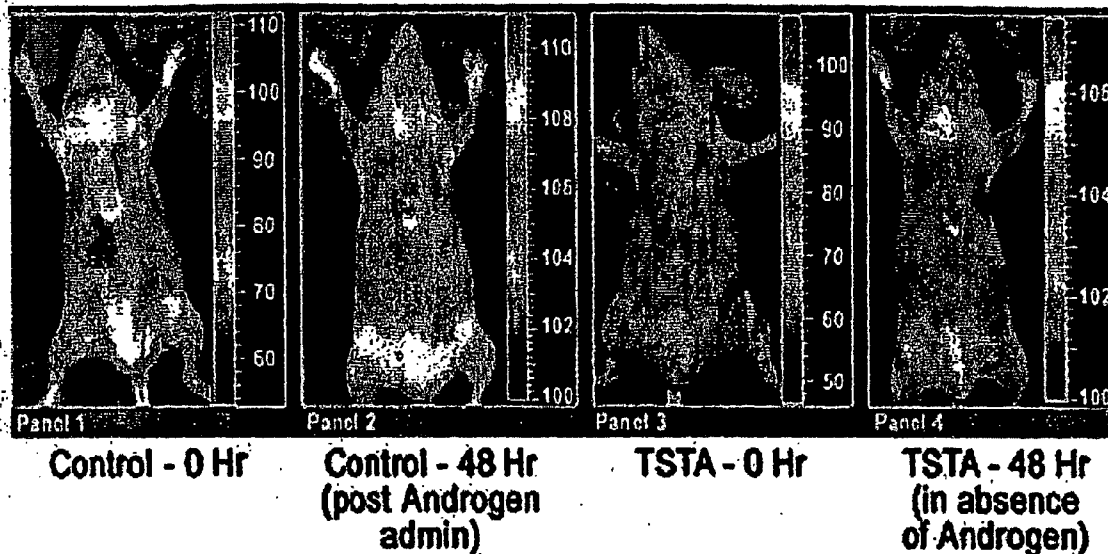


Fig. 3

A



B

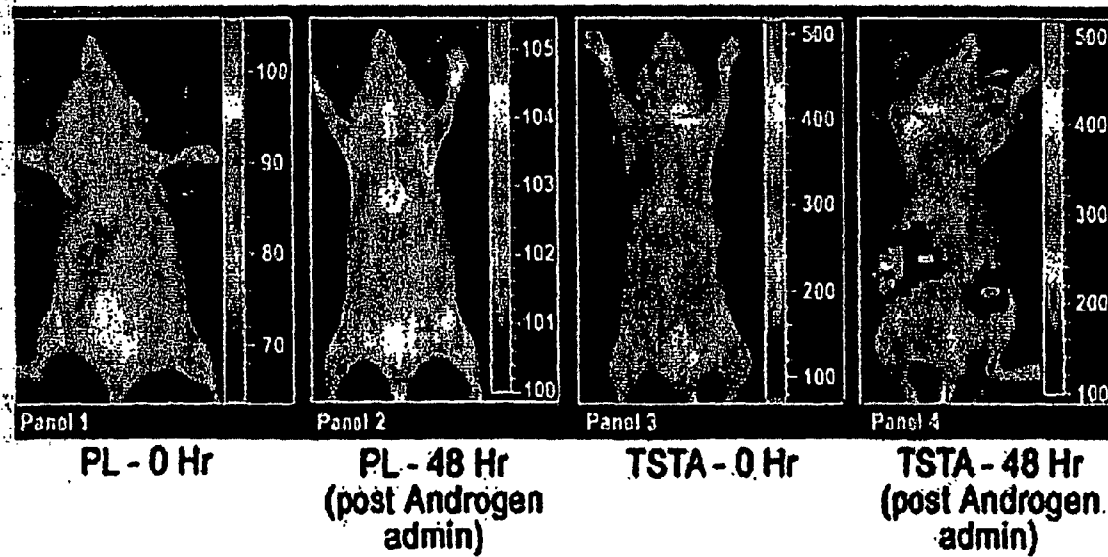


Fig. 4

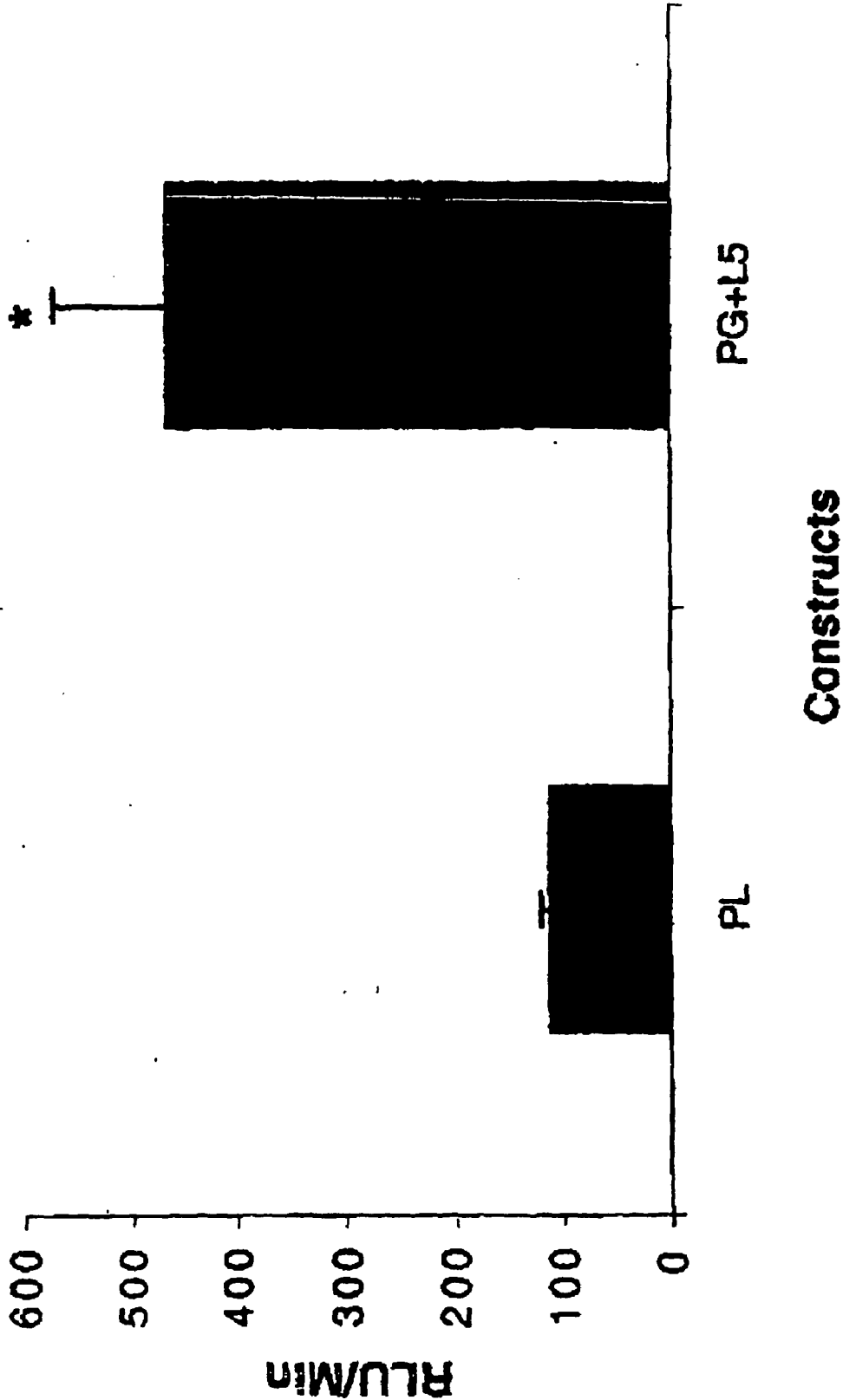


Fig. 5

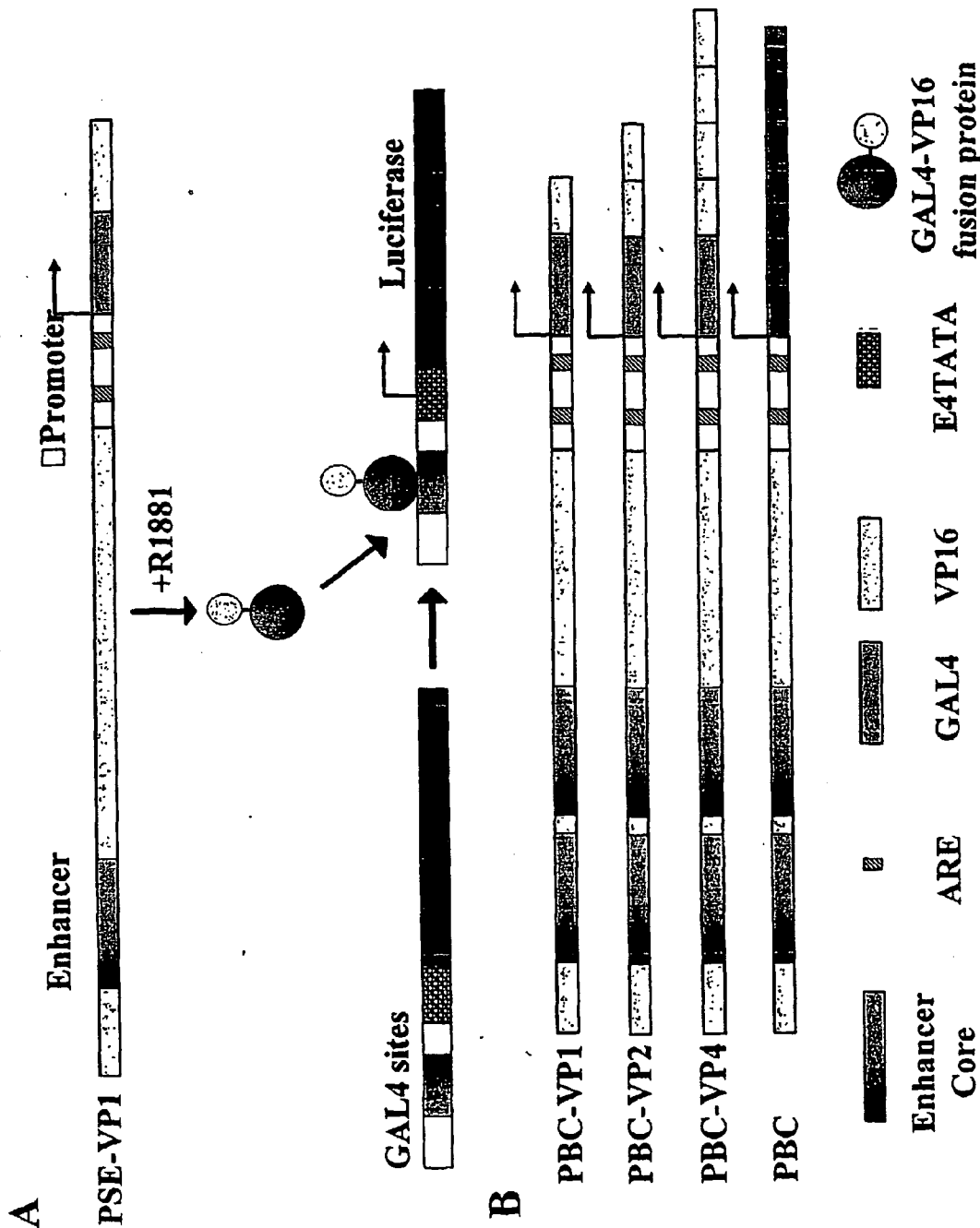


Fig. 6 -1

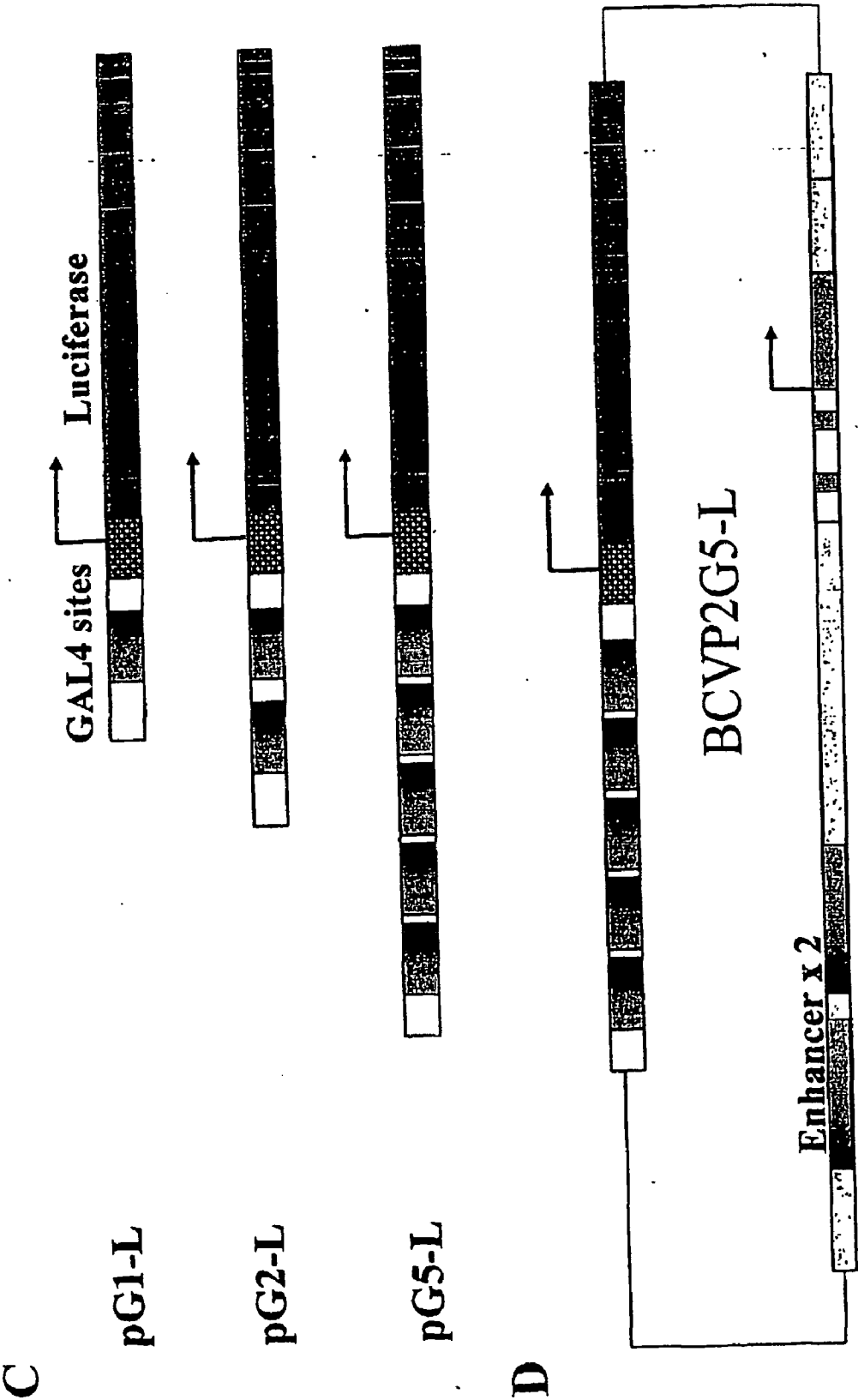


Fig. 6-2

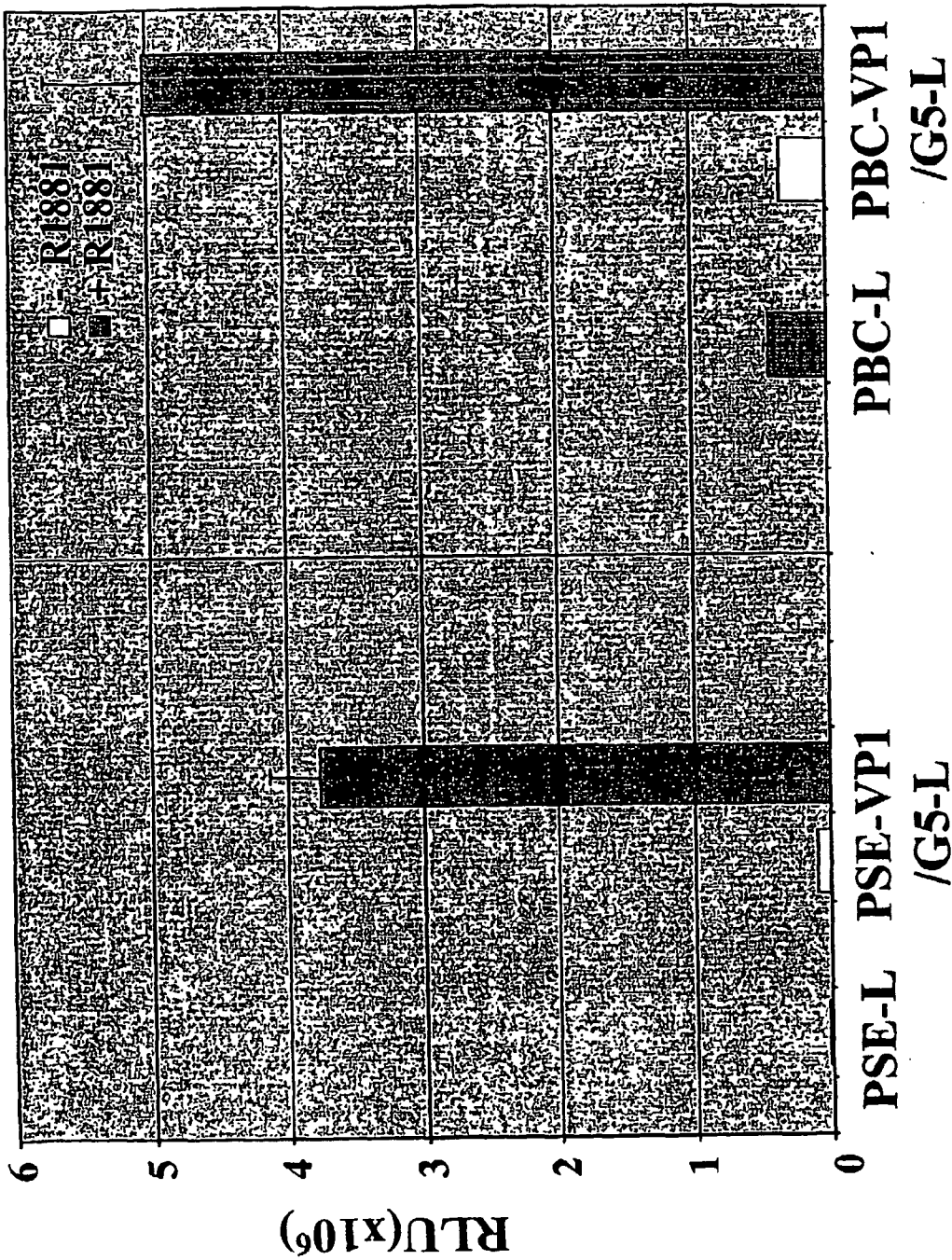


Fig. 7

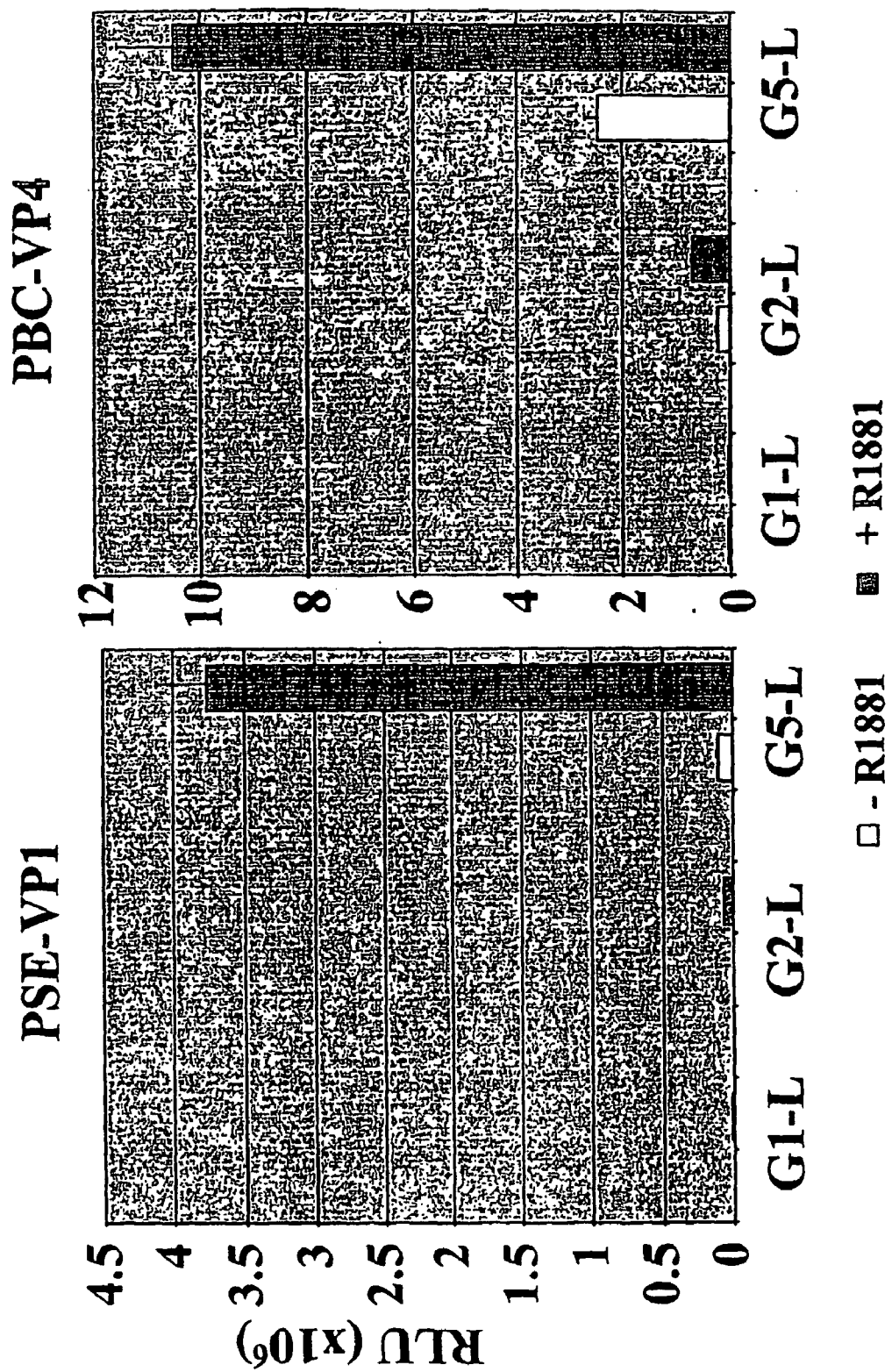


Fig. 8

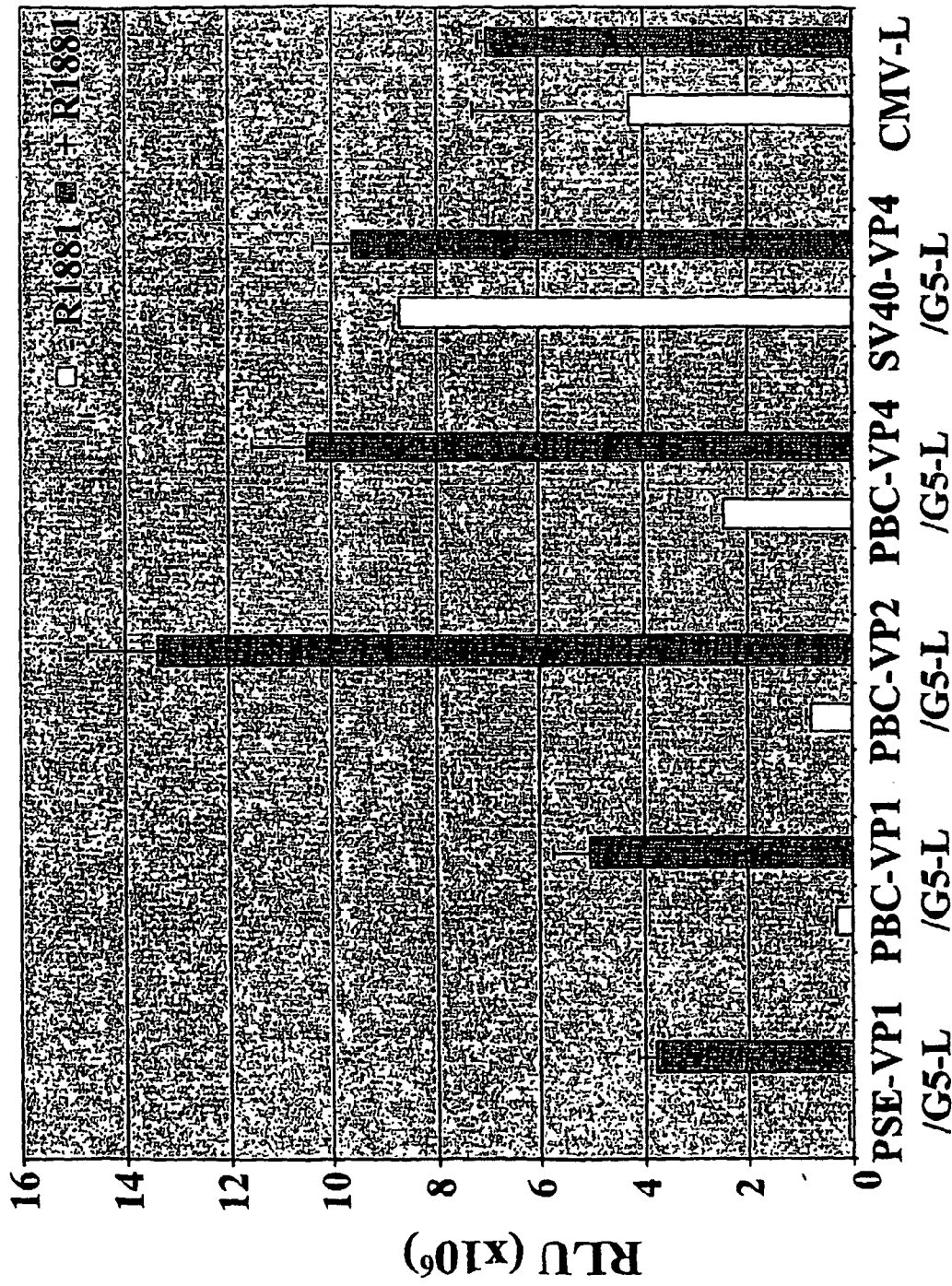


Fig. 9

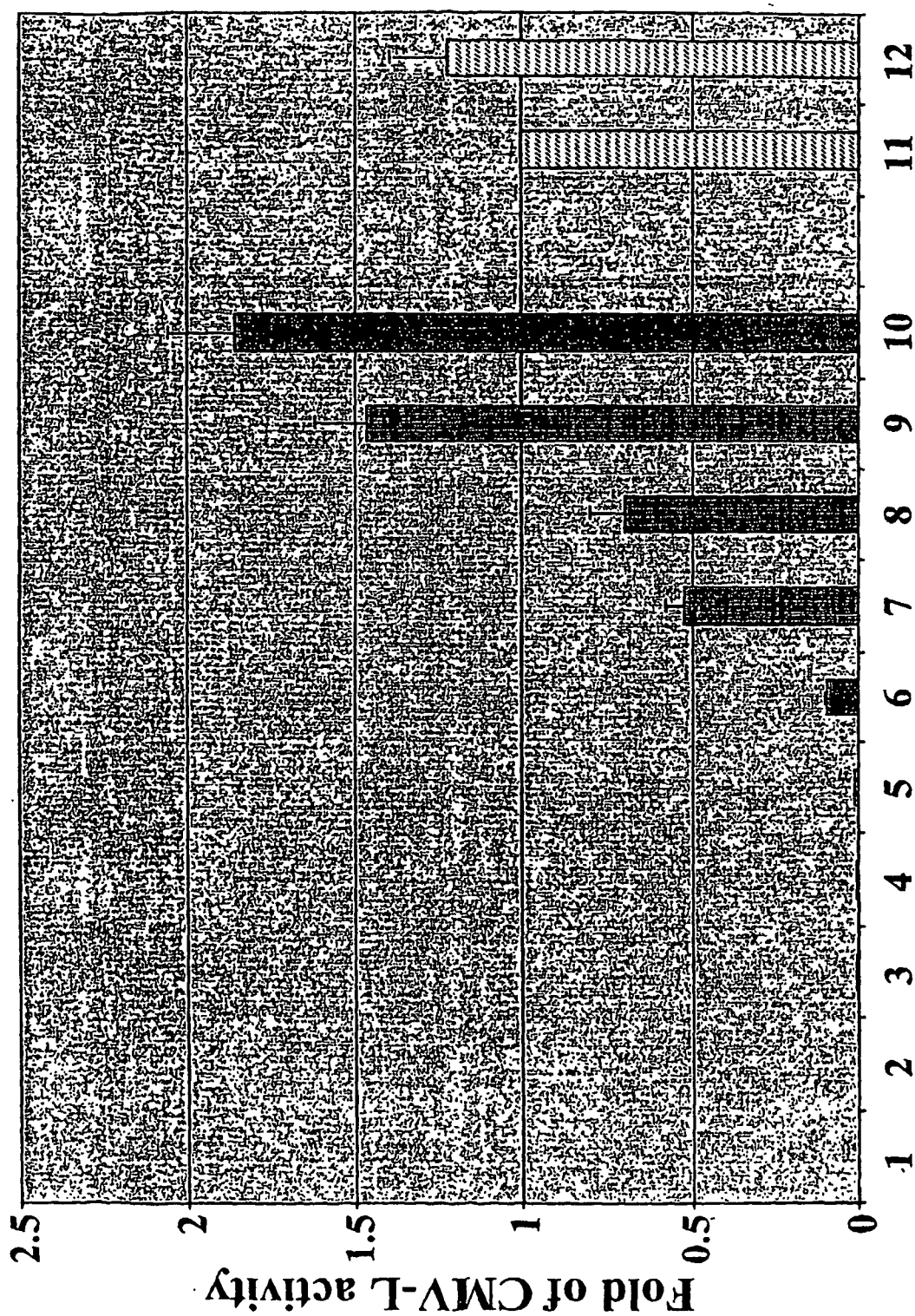


Fig. 10

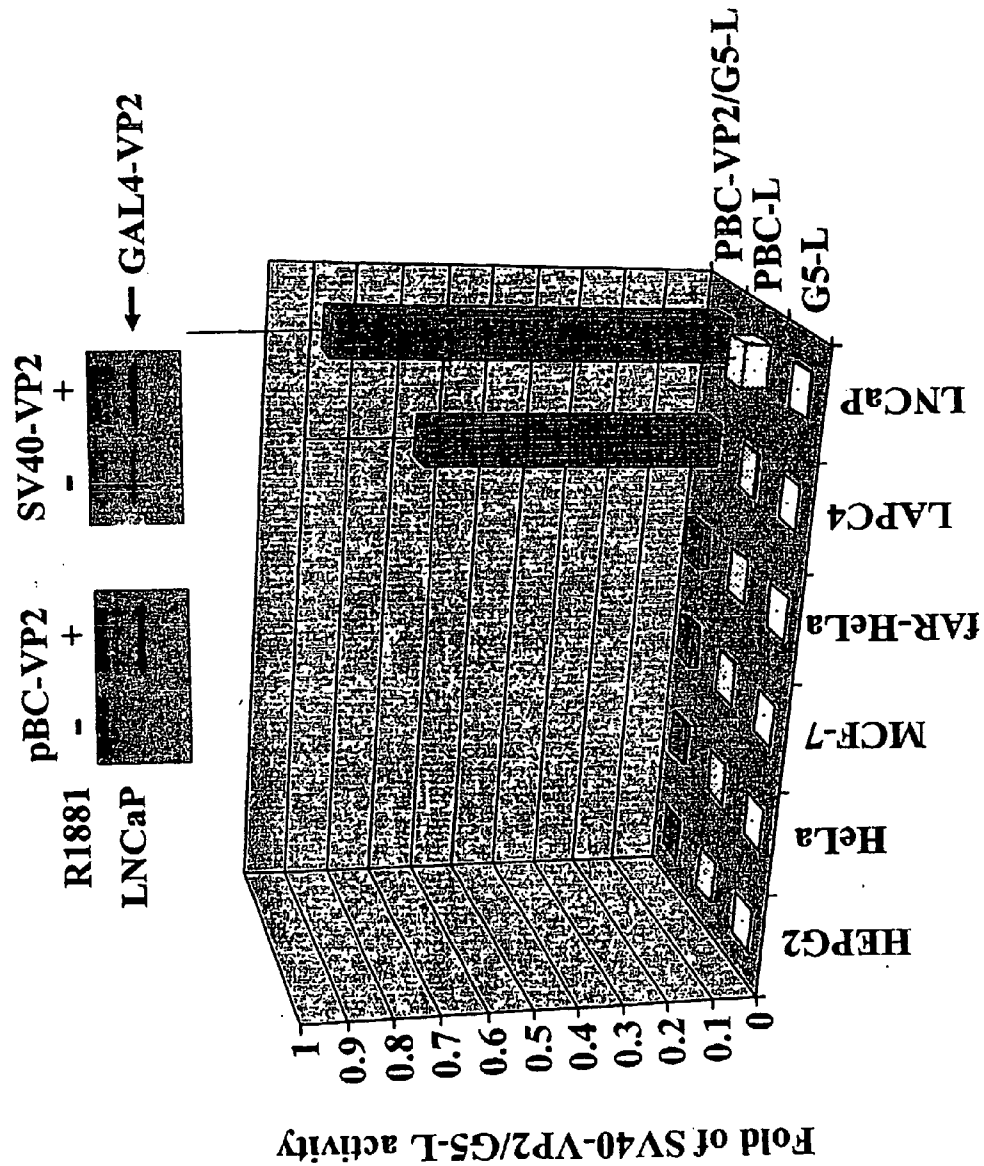


Fig. 11

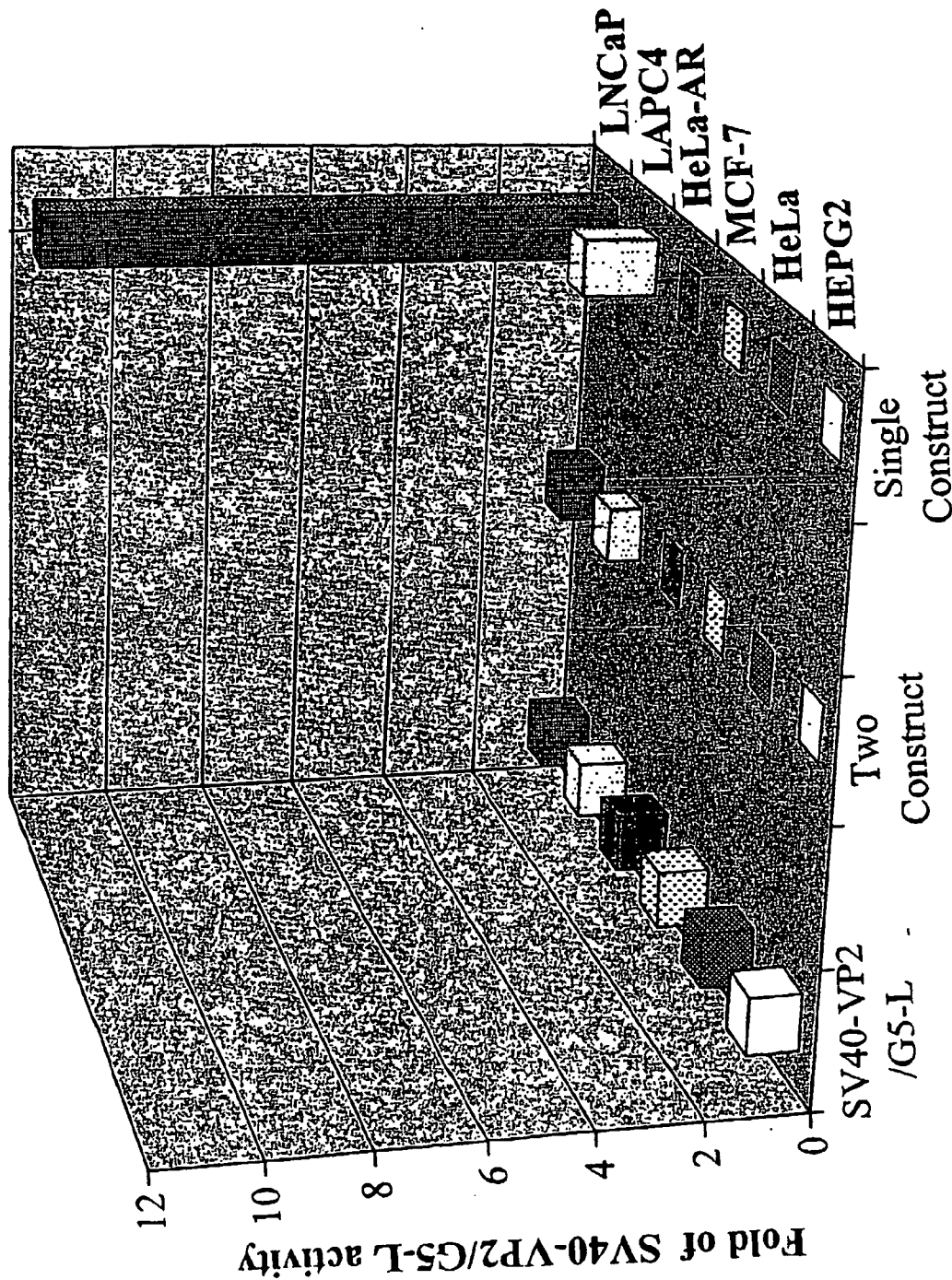
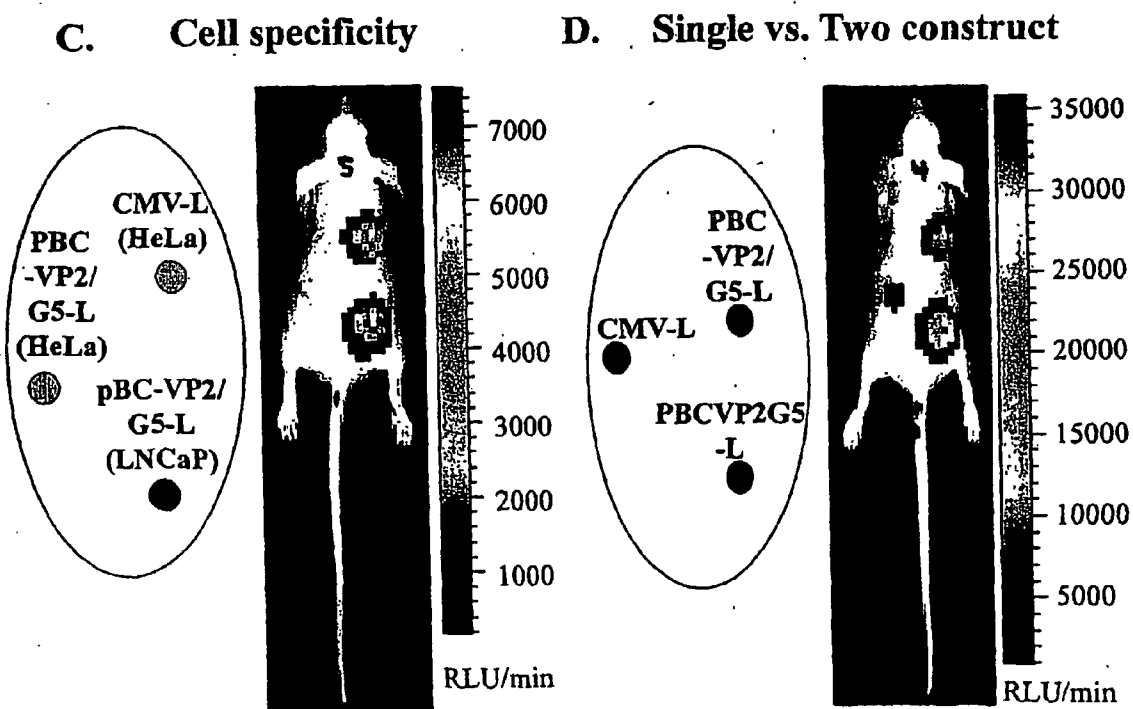
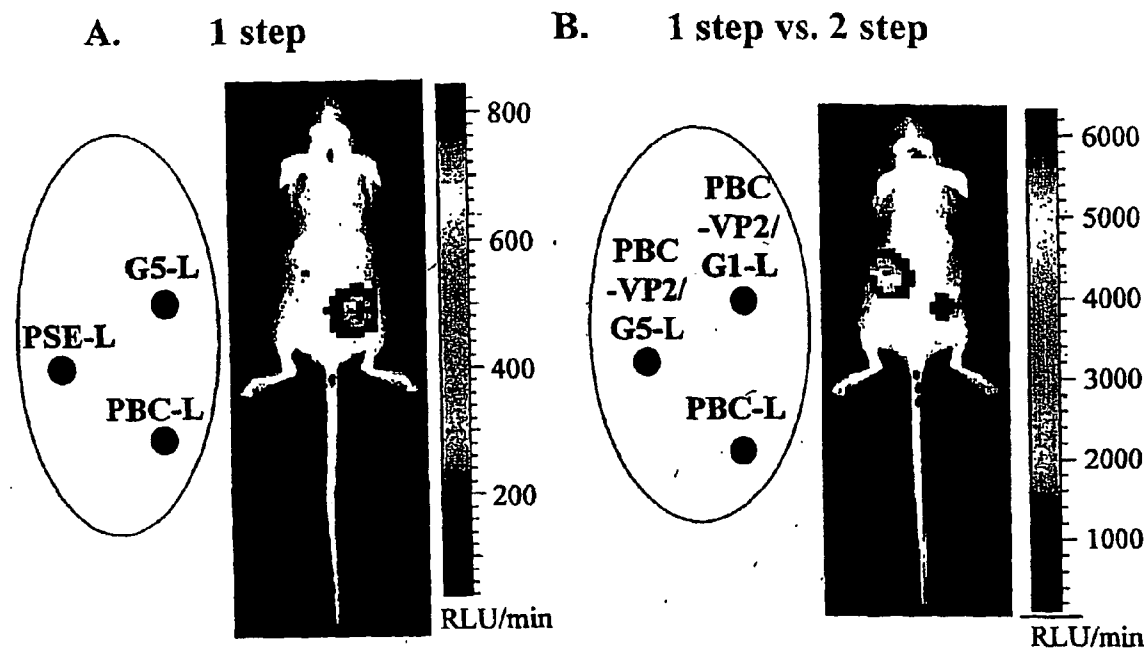


Fig. 12



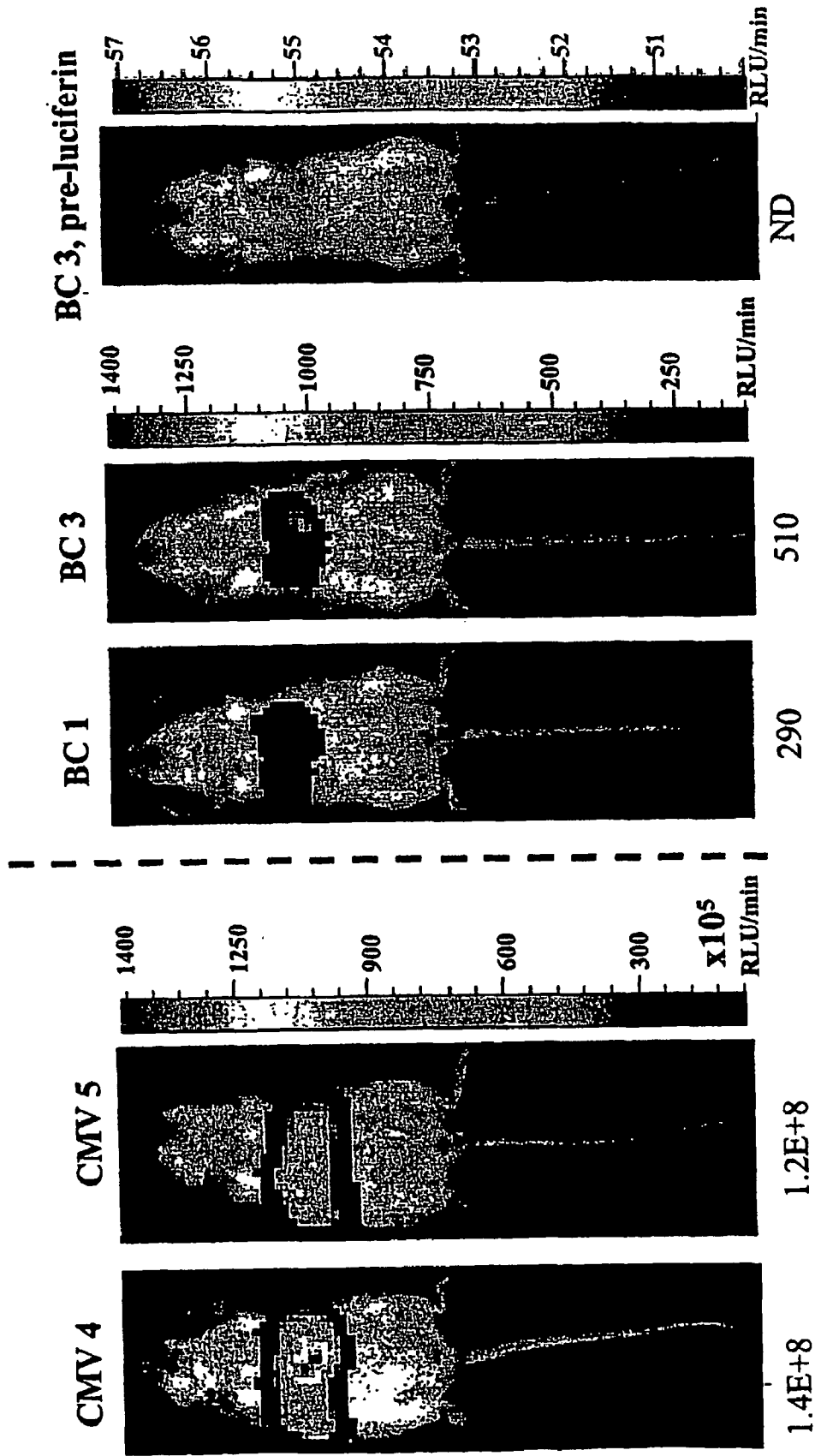


Fig. 14-1

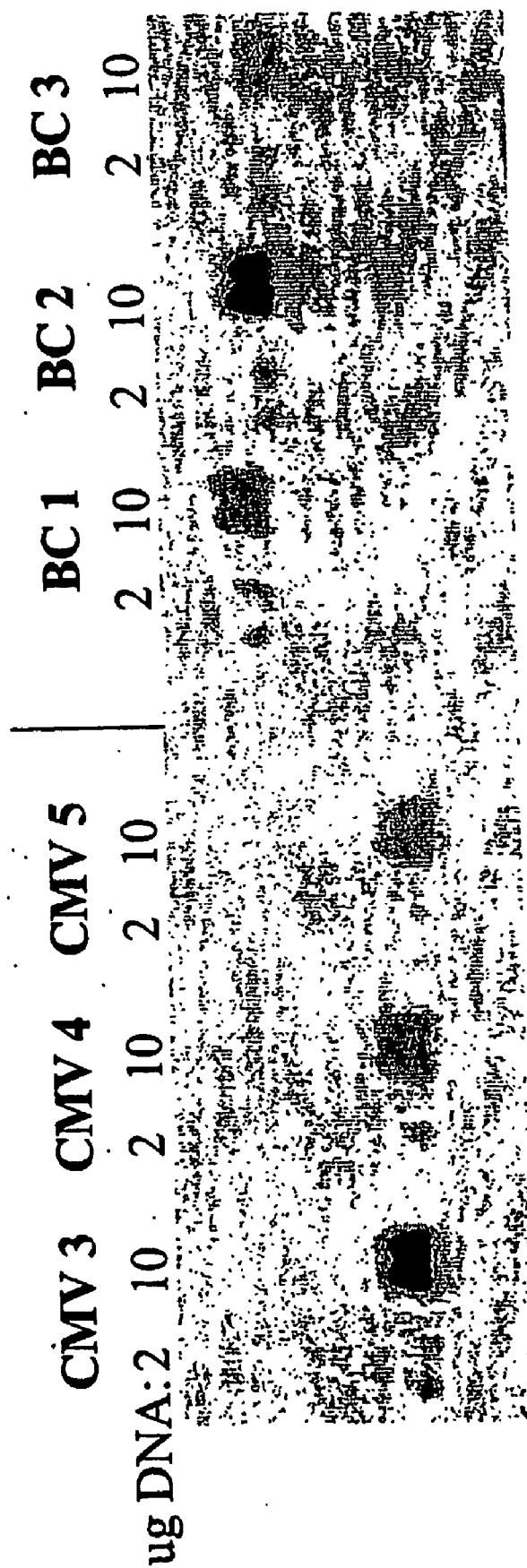


Fig. 14-2

CMV 1 (days post injection of AdCMV-luc):

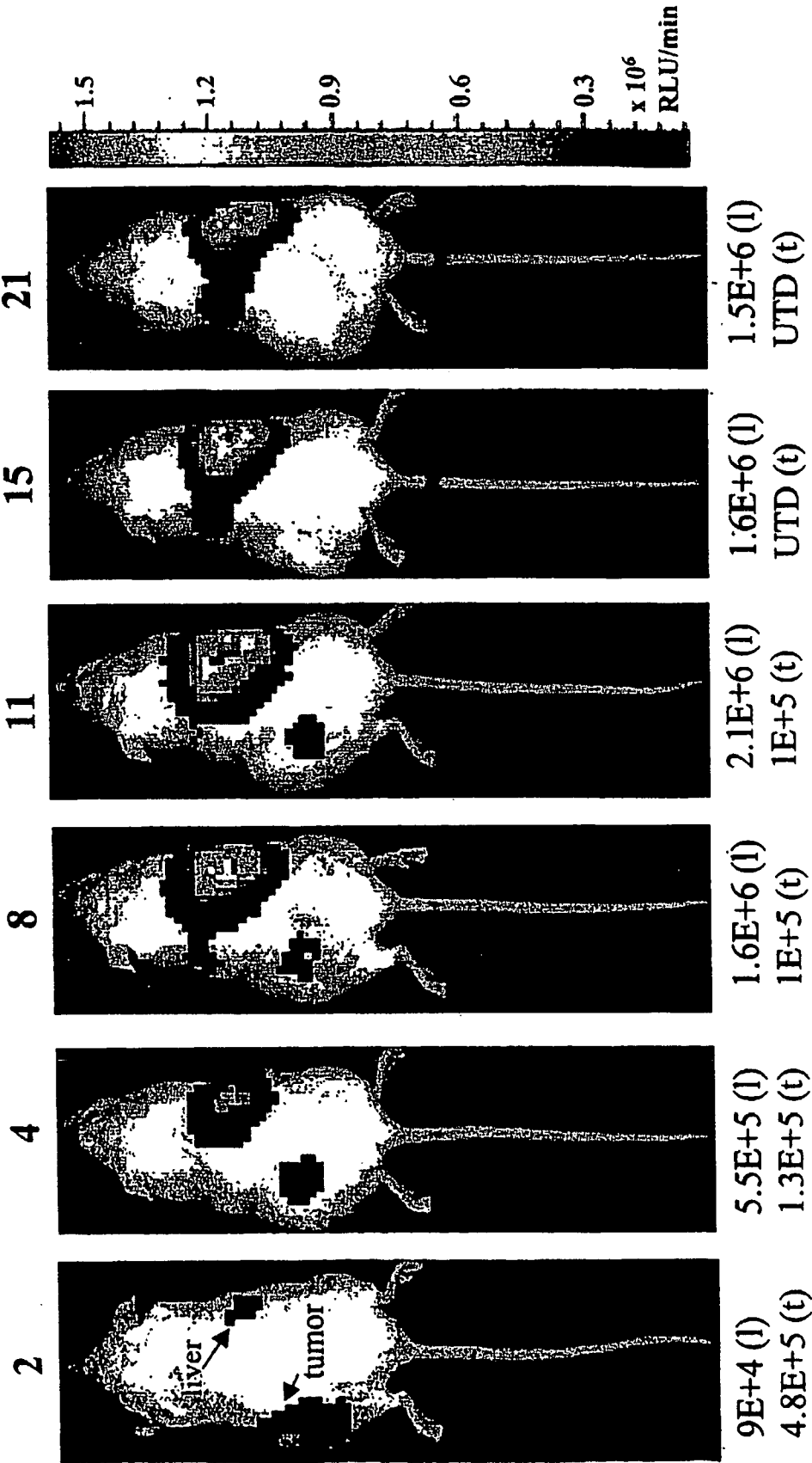


Fig. 15-1

BC4 (days post injection of AdPSE-BC-luc):

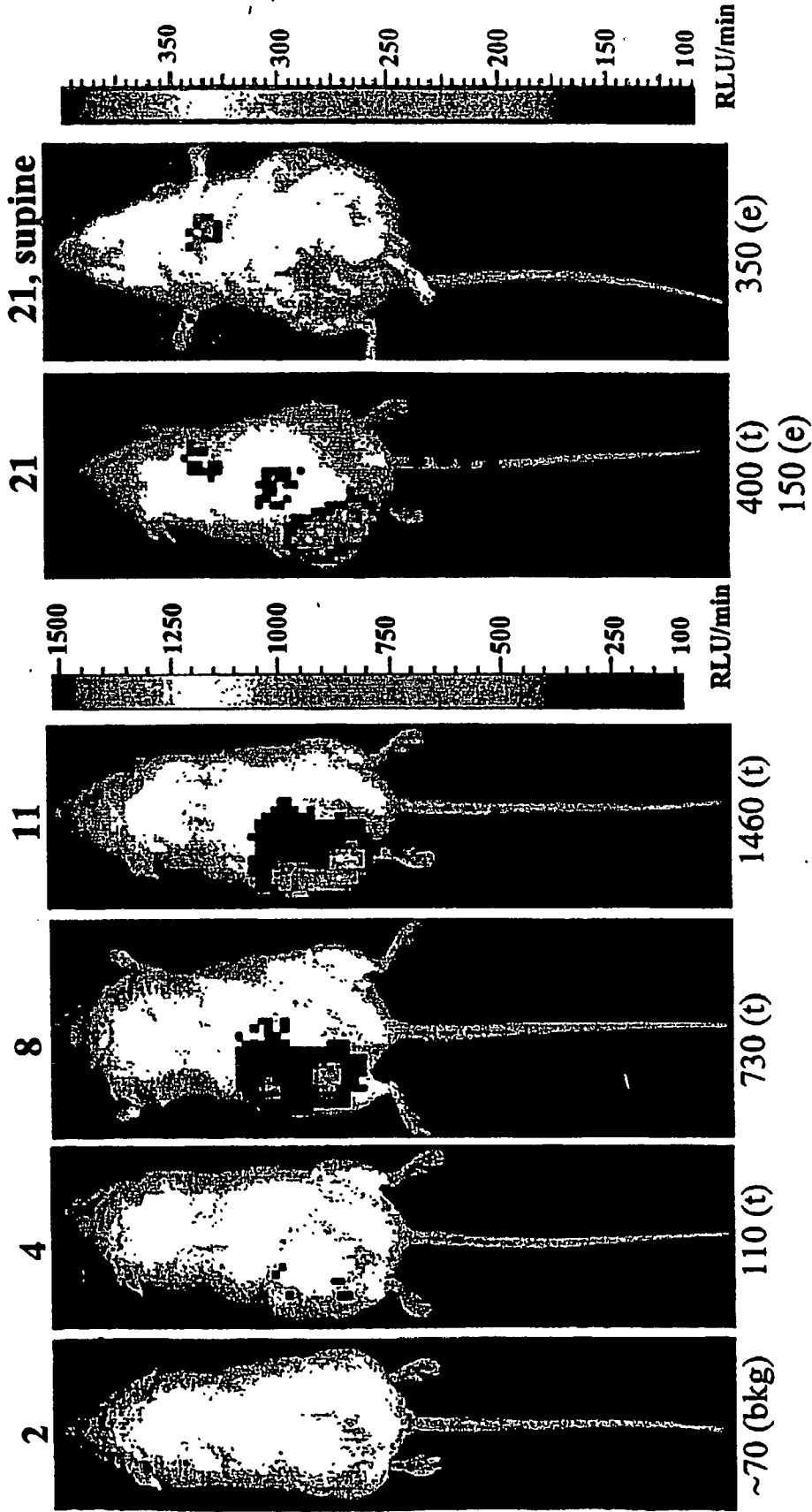


Fig. 15-2

BC 4:

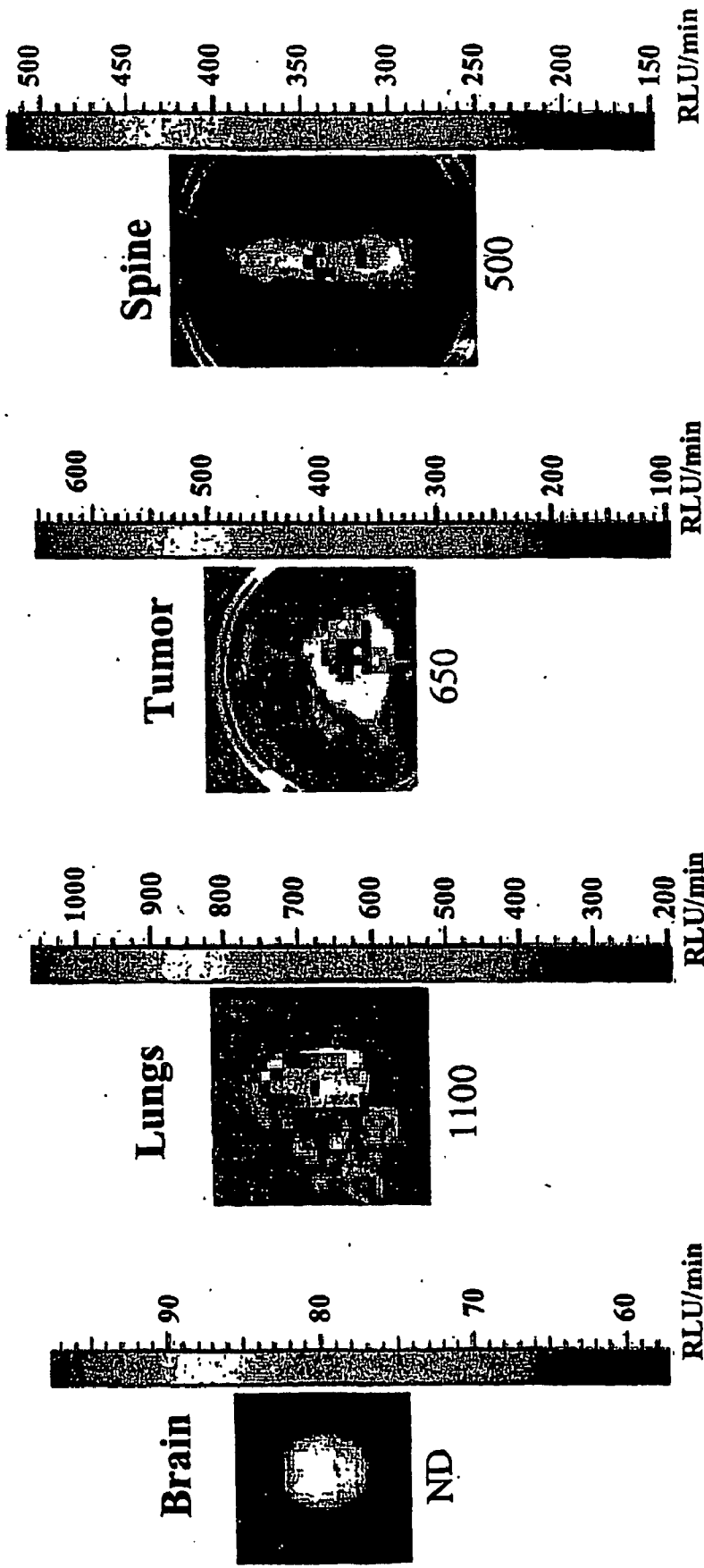


Fig. 15-3.

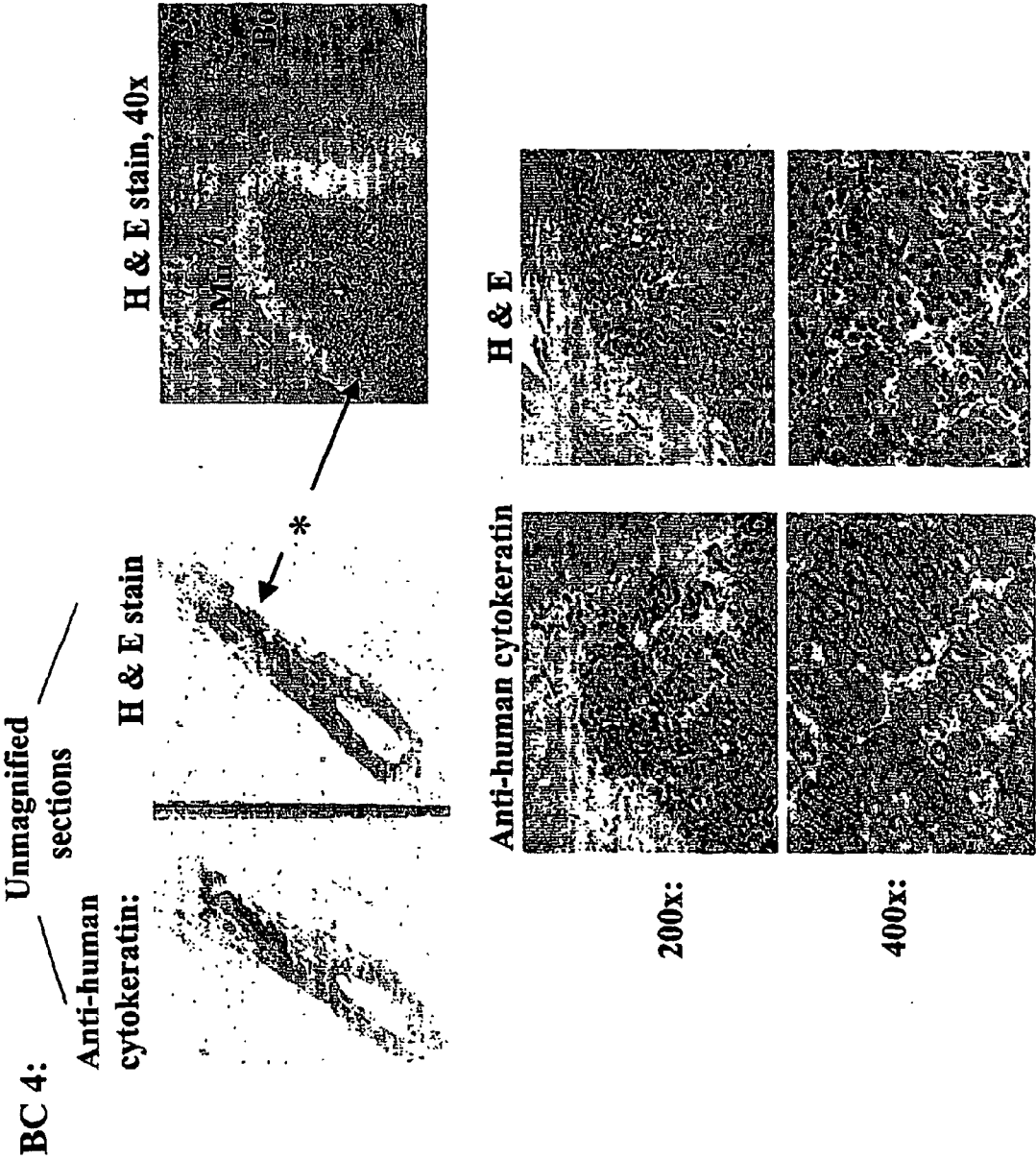
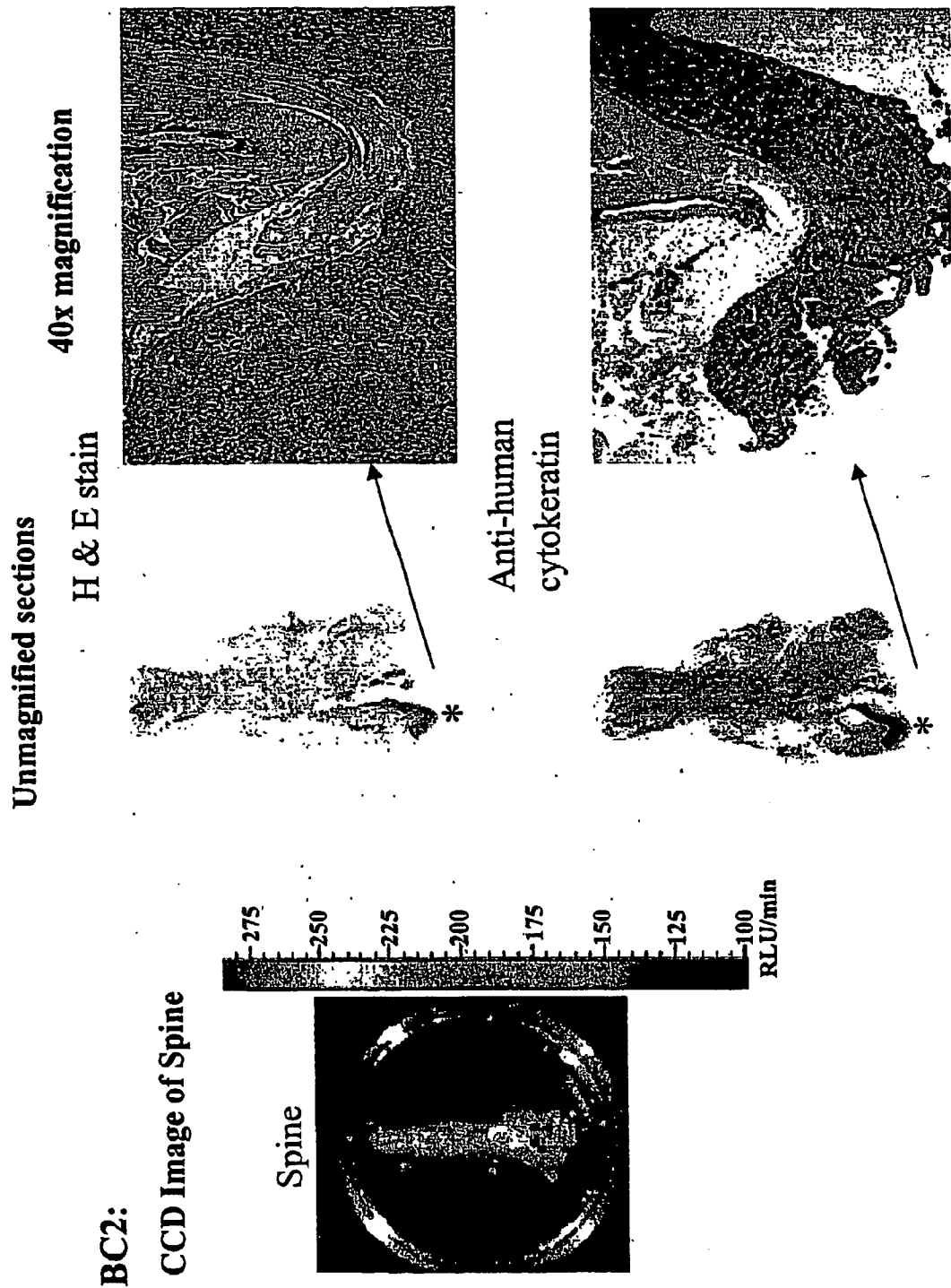


Fig. 16-1



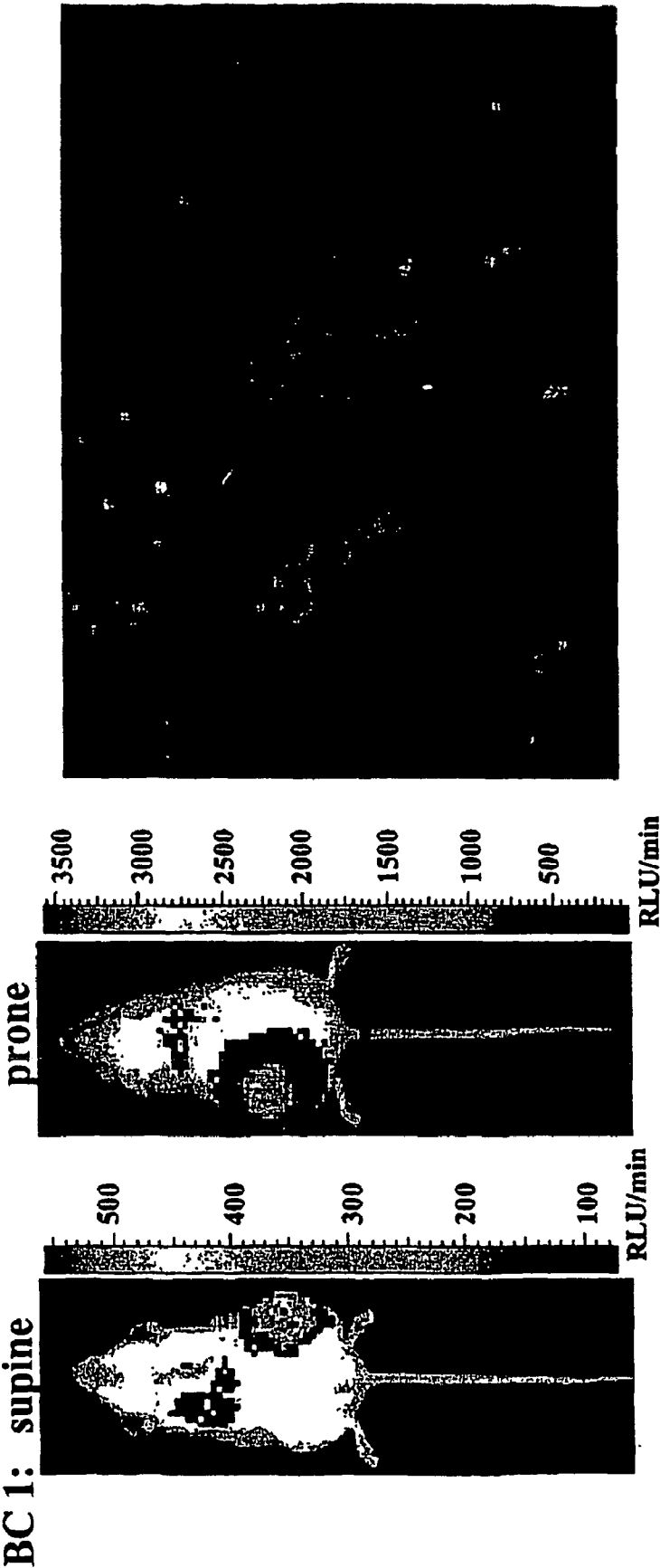
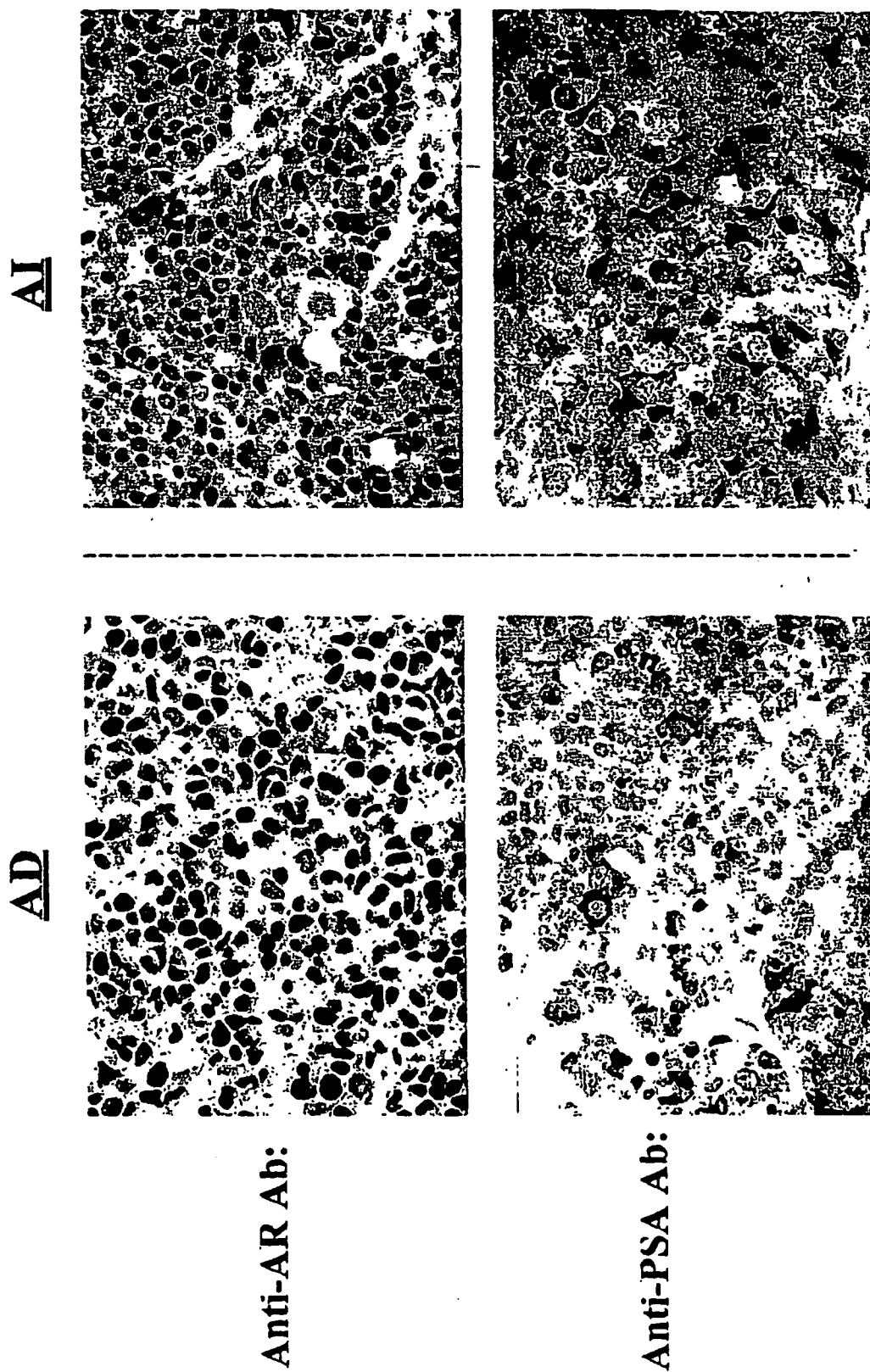


Fig. 16-3



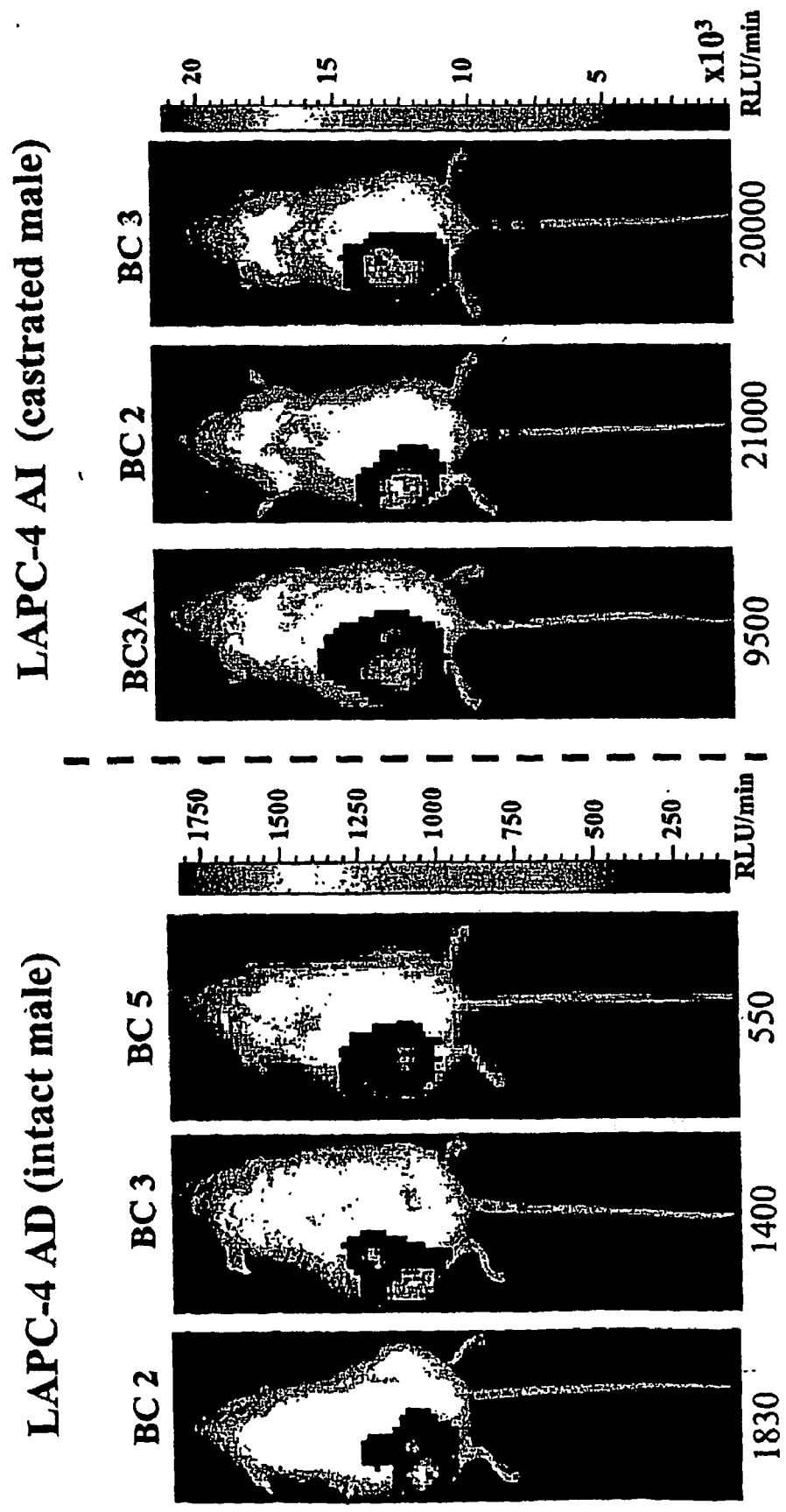


Fig. 17-2

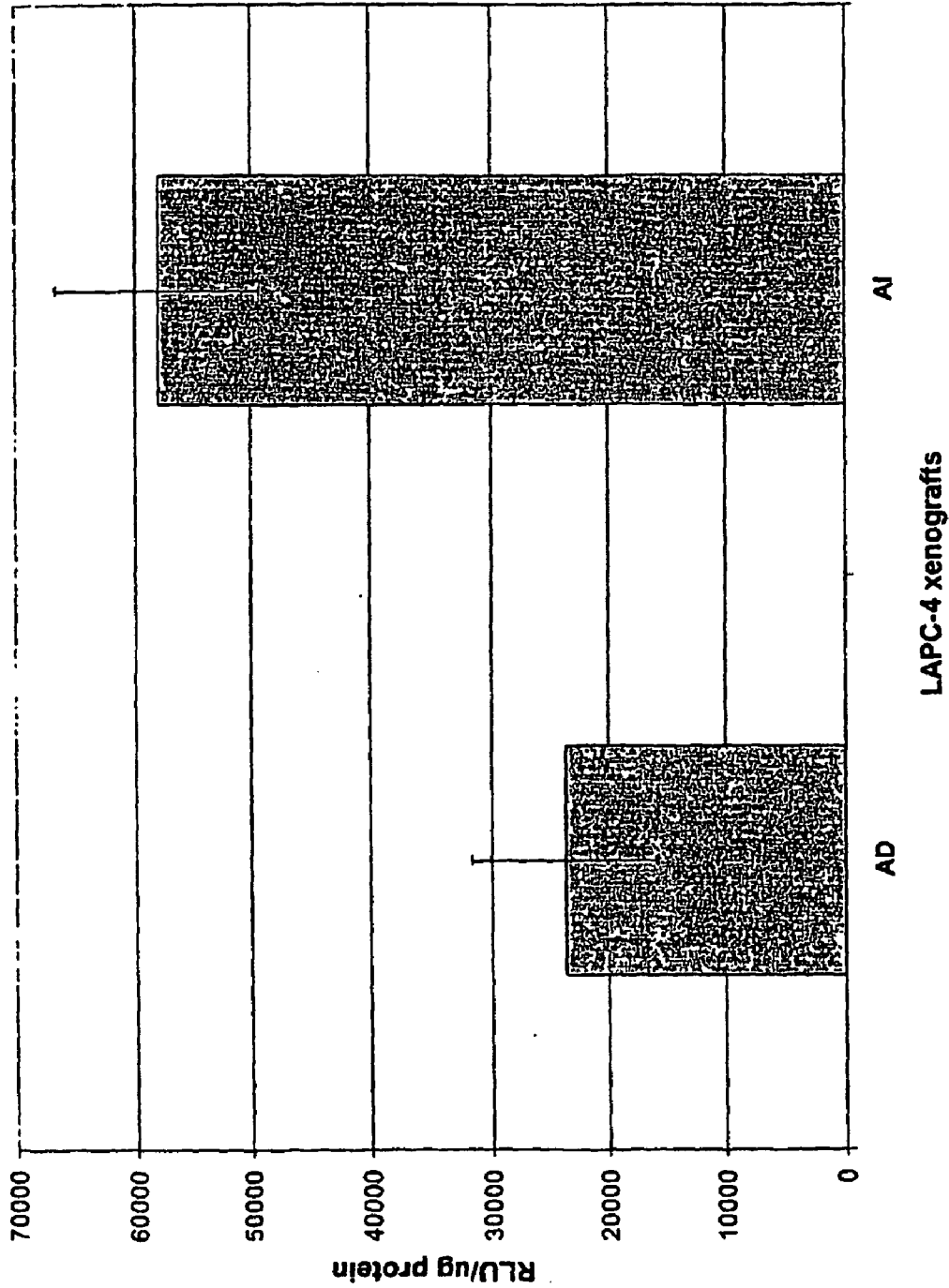


Fig. 17-3

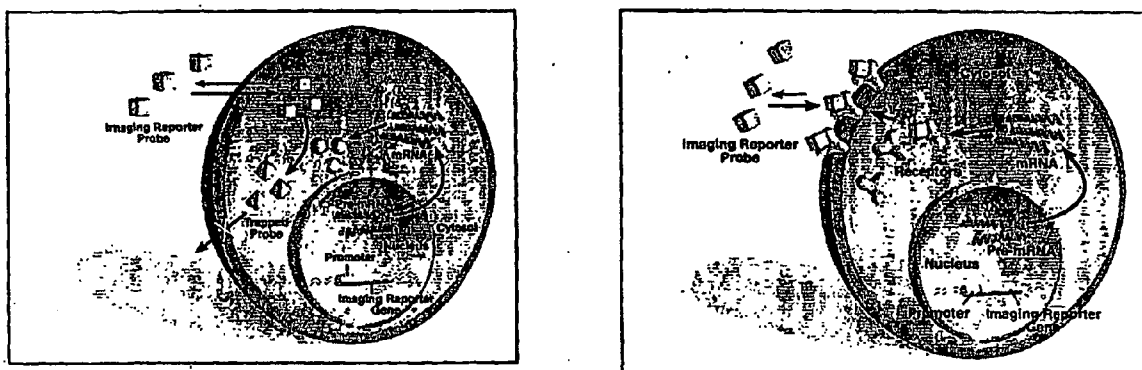


Figure 18

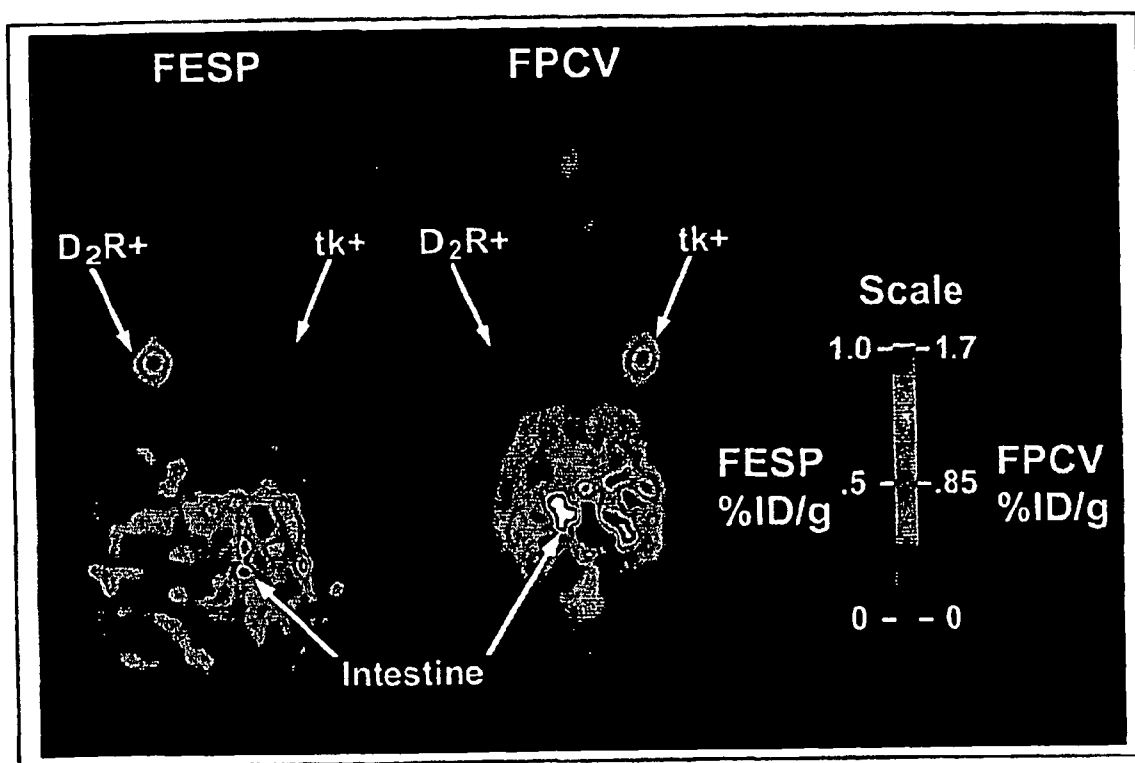


Figure 19

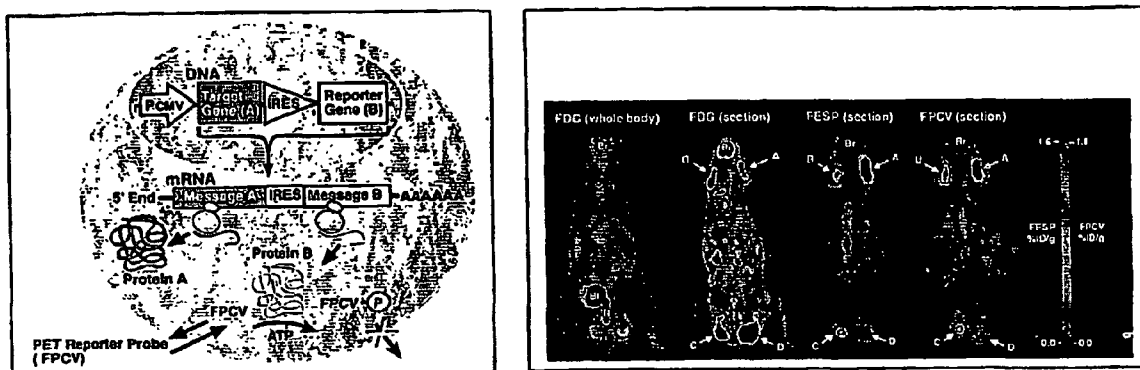


Figure 20

Pbcvp2g5 (not-sal)

KpnI
 Acc65I
 1 GGTACCGAGC TCATTTAGGT GACACTATAG AATACAAGCT TGCATGCCTG
 51 CAGGTCCGGA GGACAGTACT CCGCTCGGAG GACAGTACTC CGCTCGGAGG
 101 ACAGTACTCC GCTCGGAGGA CAGTACTCCG CTCGGAGGAC AGTACTCCGA
 XbaI BamHI
 151 CTCTAGAGGA TCCCCAGTCC TATATATACT CGCTCTGCAC TTGGCCCTTT
 BglII
 XhoI
 201 TTTACACTGT GACTGATTGA GCTGGTGCCG TGTCGAGTGG TGTCTCGAGA
 HindIII NcoI
 251 TCTGCGATCT AAGTAAGCTT GGCATTCCGG TACTGTTGGT AAAGCCACCA
 M Frame 3
 SfoI
 NarI
 KsiI
 BbeI
 301 TGGAAGACGC CAAAAACATA AAGAAAGGCC CGGCGCCATT CTATCCGCTG
 E D A K N I K K G P A P F Y P L Frame 3
 351 GAAGATGGAA CCGCTGGAGA GCAACTGCAT AAGGCTATGA AGAGATACGC
 E D G T A G E Q L H K A M K R Y A Frame 3
 401 CCTGGTTCCT GGAACAATTG CTTTACAGA TGCACATATC GAGGTGGACA
 L V P G T I A F T D A H I E V D I Frame 3
 BstBI
 451 TCACTTACGC TGAGTACTTC GAAATGTCCG TTCGGTTGGC AGAAGCTATG
 T Y A E Y F E M S V R L A E A M Frame 3
 501 AAACGATATG GGCTGAATAC AAATCACAGA ATCGTCGTAT GCAGTGAAAA
 K R Y G L N T N H R I V V C S E N Frame 3
 551 CTCTCTTCAA TTCTTTATGC CCGTGTGGG CGCGTTATTT ATCGGAGTTG
 S L Q F F M P V L G A L F I G V A Frame 3
 601 CAGTTGCGCC CGCGAACGAC ATTTATAATG AACGTGAATT GCTCAACAGT
 V A P A N D I Y N E R E L L N S Frame 3
 651 ATGGGCATTT CGCAGCCTAC CGTGGTGTTC GTTTCCAAAA AGGGGTTGCA
 M G I S Q P T V V F V S K K G L Q Frame 3
 701 AAAAATTTTG AACGTGCAAA AAAAGCTCCC AATCATCCAA AAAATTATTA
 K I L N V Q K K L P I I Q K I I I Frame 3
 BsrGI
 751 TCATGGATTC TAAAACGGAT TACCAGGGAT TTCAGTCGAT GTACACGTTT

Fig. 21A-1

M D S K T D Y Q G F Q S M Y T F Frame 3
 801 GTCACATCTC ATCTACCTCC CGGTTTAAAT GAATACGATT TTGTGCCAGA
 V T S H L P P G F N E Y D F V P E Frame 3
 BclI
 851 GTCCTTCGAT AGGGACAAGA CAATTGCACT GATCATGAAC TCCTCTGGAT
 S F D R D K T I A L I M N S S G S Frame 3
 901 CTACTGGTCT GCCTAAAGGT GTCGCTCTGC CTCATAGAAC TGCCTGCGTG
 T G L P K G V A L P H R T A C V Frame 3
 951 AGATTCTCGC ATGCCAGAGA TCCTATTTTT GGCAATCAAA TCATTCCGGA
 R F S H A R D P I F G N Q I I P D Frame 3
 1001 TACTGCGATT TTAAGTGTG TTCCATTCCA TCACGGTTTT GGAATGTTTA
 T A I L S V V P F H H G F G M F T Frame 3
 1051 CTACACTCGG ATATTGATA TGTGGATTTC GAGTCGTCTT AATGTATAGA
 T L G Y L I C G F R V V L M Y R Frame 3
 SapI
 1101 TTTGAAGAAG AGCTGTTTCT GAGGAGCCTT CAGGATTACA AGATTCAAAG
 F E E E L F L R S L Q D Y K I Q S Frame 3
 1151 TGCCTGCTG GTGCAACCC TATTCTCCTT CTTGCGCAAA AGCACTCTGA
 A L L V P T L F S F F A K S T L I Frame 3
 1201 TTGACAAATA CGATTATCT AATTACACG AAATTGCTTC TGGTGGCGCT
 D K Y D L S N L H E I A S G G A Frame 3
 1251 CCCCTCTCTA AGGAAGTCGG GGAAGCGGTT GCCAAGAGGT TCCATCTGCC
 P L S K E V G E A V A K R F H L P Frame 3
 1301 AGGTATCAGG CAAGGATATG GGCTCACTGA GACTACATCA GCTATTCTGA
 G I R Q G Y G L T E T T S A I L I Frame 3
 1351 TTACACCCGA GGGGGATGAT AAACCGGGCG CGGTCGGTAA AGTTGTTCCA
 T P E G D D K P G A V G K V V P Frame 3
 1401 TTTTTTGAAG CGAAGGTTGT GGATCTGGAT ACCGGGAAAA CGCTGGGCGT
 F F E A K V V D L D T G K T L G V Frame 3
 1451 TAATCAAAGA GCGAACTGT GTGTGAGAGG TCCTATGATT ATGTCCGGTT
 N Q R G E L C V R G P M I M S G Y Frame 3
 1501 ATGTAAACAA TCCGGAAGCG ACCAACGCCT TGATTGACAA GGATGGATGG
 V N N P E A T N A L I D K D G W Frame 3
 1551 CTACATTCTG GAGACATAGC TTACTGGGAC GAAGACGAAC ACTTCTTCAT
 L H S G D I A Y W D E D E H F F I Frame 3
 1601 CGTTGACCGC CTGAAGTCTC TGATTAAGTA CAAAGGCTAT CAGGTGGCTC
 V D R L K S L I K Y K G Y Q V A P Frame 3
 1651 CCGCTGAATT GGAATCCATC TTGCTCCAAC ACCCCAACAT CTTGACGCA
 A E L E S I L L Q H P N I F D A Frame 3

Fig. 21A-2

SgrAI

1701 GGTGTCGCAG GTCTTCCCGA CGATGACGCC GGTGAACTTC CCGCCGCCGT
G V A G L P D D D A G E L P A A V Frame 3

1751 TGTGTGTTTG GAGCACGGAA AGACGATGAC GGAAAAAGAG ATCGTGGATT
V V L E H G K T M T E K E I V D Y Frame 3

1801 ACGTCGCCAG TCAAGTAACA ACCGCGAAAA AGTTGCGCGG AGGAGTTGTG
V A S Q V T T A K K L R G G V V Frame 3

1851 TTTGTGGACG AAGTACCGAA AGGTCTTACC GGAAACTCG ACGCAAGAAA
F V D E V P K G L T G K L D A R K Frame 3

1901 AATCAGAGAG ATCCTCATAA AGGCCAAGAA GGGCGGAAAG ATCGCCGTGT
I R E I L I K A K K G G K I A V * Frame 3

XbaI FseI

1951 AATTCTAGAG TCGGGGCGGC CGGCCGCTTC GAGCAGACAT GATAAGATAC

2001 ATTGATGAGT TTGGACAAAC CACAAC TAGA ATGCAGTGAA AAAAATGCTT

2051 TATTTGTGAA ATTTGTGATG CTATTGCTTT ATTTGTAACC ATTATAAGCT

2101 GCAATAAACA AGTTAACAAC AACAAATTGCA TTCATTTTAT GTTTCAGGTT

2151 CAGGGGGAGG TGTGGGAGGT TTTTAAAGC AAGTAAACC TCTACAAATG

Sali
BamHI AccI

2201 TGGTAAATC GATAAGGATC CGTCGACCGA TGCCCTTGAG AGCCTTCAAC

2251 CCAGTCAGCT CCTTCCGGTG GGCGCGGGGC ATGACTATCG TCGCCGCACT

SapI
AfeI

2301 TATGACTGTC TTCTTTATCA TGCAACTCGT AGGACAGGTG CCGGCAGCGC

2351 TCTTCCGCTT CCTCGCTCAC TGACTCGCTG CGCTCGGTG TTCGGCTGCG

2401 GCGAGCGGTA TCAGCTCACT CAAAGGCGGT AATACGGTTA TCCACAGAA

2451 CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAGGCC

2501 AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCCC

2551 CCCTGACGAG CATCAGAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC

BssSI

2601 CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG

2651 CGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT

2701 CCCTTCGGGA AGCGTGGCGC TTTCTCAATG CTCACGCTGT AGGTATCTCA

2751 GTTCGGTGTA GGTGTTTCG TCCAAGCTGG GCTGTGTGCA CGAACCCCCC

Fig. 21A-3

2801 GTTCAGCCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA
2851 CCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA
2901 TTAGCAGAGC GAGGTATGTA GCGGGTGCTA CAGAGTTCTT GAAGTGGTGG
2951 CCTAACTACG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT
3001 GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA TCCGGCAAAC
3051 AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG
3101 CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC
3151 TGACGCTCAG TGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT
3201 TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTTT
3251 AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG
* W H Frame 4

3301 CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA
K I L S A G I E A I Q R N R E D Frame 4

AhdI
3351 TAGTTGCC TG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA
M T A Q S G T T Y I V V I R S P K Frame 4

3401 CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC
G D P G L A A I I G R S G R E G A Frame 4

BglI
3451 TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA
G S K D A I F W G A P L A S R L Frame 4

AseI
3501 GTGGTCTGTC AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG
L P G A V K D A E M W D I L Q Q R Frame 4

FspI
3551 GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC
S A L T L L E G T L L K R L T T A Frame 4

3601 CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT
M A V P M T T D R E D N P I A E Frame 4

3651 TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG
N L E P E W R D L R T V H D G M N Frame 4

3701 TGCAAAAAAG CGGTTAGCTC CTTCCGTCCT CCGATCGTTG TCAGAAGTAA
H L F A T L E K P G G I T T L L L Frame 4

3751 GTTGGCCGCA GTGTTATCAC TCATGGTIAT GGCAGCACTG CATAATTCTC
N A A T N D S M T I A A S C L E Frame 4

3801 TTA CTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA
R V T M G D T L H K E T V P S Y E Frame 4

Fig. 21A-4

3951 ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC
V L D N Q S Y H I R R G L Q E Q G Frame 4

3901 GGCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT TTAAAAGTGC
A D I R S L V A G C L L V K F T Frame 4

XmnI
3951 TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG
S M M P F R E E P R F S E L I K G Frame 4

BssSI
4001 CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC
S N L D L E I Y G V R A G L Q D E Frame 4

4051 AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC
A D K V K V L T E P H A F V P L Frame 4

4101 AAAATGCCGC AAAAAGGGA ATAAGGGCGA CACGGAAATG TTGAATACTC
C F A A F F P I L A V R F H Q I S Frame 4

4151 ATACTCTTCC TTTTCAATA TTATTGAAGC ATTTATCAGG GTTATTGTCT
M Frame 4

4201 CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG

4251 TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGCGCC CTGTAGCGGC

4301 GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT

4351 TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG

4401 CCACGTTCCG CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA

4451 GGGTTCGGAT TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA

DraIII
4501 GGGTGATGGT TCACGTAGTG GGCCATCGCC CTGATAGACG GTTTTTCGCC

AloI
AloI
4551 CTTTGACGTT GGAGTCCACG TTCTTTAATA GTGGACTCTT GTTCCAAACT

4601 GGAACAACAC TCAACCCTAT CTCGGTCTAT TCTTTTGATT TATAAGGGAT

4651 TTTGCCGATT TCGGCCTATT GGTAAAAAAA TGAGCTGATT TAACAAAAAT

BglI
4701 TTAACGCGAA TTTTAACAAA ATATTAACGT TTACAATTC CCATTGCCA

FspI
4751 TTCAGGCTGC GCAACTGTTG GGAAGGGCGA TCGGTGCGGG CCTCTTCGCT

4801 ATTACGCCAG CCAAGCTAC CATGATAAGT AAGTAATATT AAGGTACGGG

NotI
4851 AGGTACTTGG AGCGGCCGCG ATCCAGACAT GATAAGATAC ATTGATGAGT

Fig. 21A-5

4301 TTGGACAAAC CACAAC TAGA ATGCACTGAA AAAAATGCTT TATTTGTGAA .
4951 ATTTGTGATG CTATTGCTTT ATTTGTAACC ATTATAAGCT GCAATAAACA
5001 AGTTAACAAC AACAAATGCA TTCATTTTAT GTTTCAGGTT CAGGGGGAGG
5051 TGTGGGAGGT TTTTAAAGC AAGTAAACC TCTACAAATG TGGTATGGCT
BclI
5101 GATTATGATC ATGAACAGAC TGTGAGGACT GAGGGGCCTG AAATGAGCCT
5151 TGGGACTGTG AATTTAAAT ACACAAACAA TTAGAATCAG TAGTTTAACA
5201 CATTATACAC TTAAAAATT TATATTTACC TTAGAGCTTT AAATCTCTGT
5251 AGGTAGTTTG TCCAATTATG TCACACCACA GAAGTAAGGT TCCTTCACAA
* T V G C F Y P E K V Frame 4
XbaI
5301 AGATCCCAAG CTGTCGATCG ACATTTCTAG AGGATCTCGG ACCCGGGGAA
F I G L Q R D V N R S S R P G P S Frame 4
5351 TCCCCGTCCC CCAACATGTC CAGATCGAAA TCGTCTAGCG CGTCGGCATG
D G D G L M D L D F D D L A D A H Frame 4
BtrI
5401 CGCCATCGCC ACGTCCTCGC CGTCTAAGTG GAGCTCGTCC CCCAGGCTGA
A M A V D E G D L H L E D G L S Frame 4
5451 CATCGGTCGG GGGGGCGGAT CTCGGACCCG GGAATCCCC GTCCCCAAC
V D T P P A S R P G P S D G D G L Frame 4
BtrI
5501 ATGTCCAGAT CGAAATCGTC TAGCGCGTCG GCATGCGCCA TCGCCACGTC
M D L D F D D L A D A H A M A V D Frame 4
5551 CTCGCCGTCT AAGTGGAGCT CGTCCCCCAG GCTGACATCG GTCGGGGGGG
E G D L H L E D G L S V D T P P Frame 4
BamHI EcoRI
5601 CGGATCCCC GGGCTGCAGG AATTCGGCG ATACAGTCAA CTGTCTTTGA
A S G G P Q L F E P S V T L Q R Q Frame 4
5651 CCTTTGTTAC TACTCTCTC CGATGATGAT GTCGCACTTA TTCTATGCTG
G K N S S E E S S S T A S I R H Q Frame 4
5701 TCTCAATGTT AGAGGCATAT CAGTCTCCAC TGAAGCCAAT CTATCTGTGA
R L T L P M D T E V S A L R D T Frame 4
BsrGI
5751 CGGCATCTTT ATTACATTA TCTTGACAA ATAATCCTGT TAACAATGCT
V A D K N V N D Q V F L G T L L A Frame 4
XhoI
5801 TTTATATCCT GTAAAGAATC CATTTCAAA ATCATGTCAA GGTCTTCTCG
K I D Q L S D M K L I M D L D E R Frame 4

Fig. 21A-6

5851 AGGAAAAATC AGTAGAAATA GCTGTTCCAG TCTTTCTAGC CTTGATTCCA
P F I L L F L Q E L R E L R S E Frame 4

5901 CTTCTGTCAG ATGTGCCCTA GTCAGCGGAG ACCTTTTGGT TTTGGGAGAG
V E T L H A R T L P S R K T K P S Frame 4

5951 TAGCGACACT CCCAGTTGTT CTTCAGACAC TTGGCGCACT TCGGTTTTTC
Y R C E W N N K L C K A C K P K E Frame 4

6001 TTTGGAGCAC TTGAGCTTTT TAAGTCGGCA AATATCGCAT GCTTGTTTGA
K S C K L K K L R C I D C A Q E Frame 4

HindIII
6051 TAGAAGACAG TAGCTTCATC TTTCAGGAGG CTTGCTTCAA GCTTGGGGCT
I S S L L K M Frame 4

6101 GGGGAGCCTC CCCCAGGAGC CCTATAAAAC CTTCATTTCC CAGGACTCCG

BglI BstXI
6151 CCCCTGCCCT GCTGGCACCC AGAGGCTGAC CAAGGCCCTC CCCATGCTGC

BstXI
6201 TGGAGGCTGG ACAACCCCCT CCCACACCCA GAGCTGTGGA AGGGGAGGGA

PsrI
PsrI
6251 GAGCTAGTAC TTGCTGTTCT GCAATTACTA GATCACCCTG GATGCACCAG

6301 GCCCTGTGGC TCATGGAGAC TTCATCTAGG GGACAAAGGC AGAGGAGACA

6351 CGCCCAGGAT GAAACAGAAA CAGGGGGTGG GTACGATCCC CGATTCTTCA

PmlI
6401 TACAAAGCCT CACGTGCCTA GATCCTTTGC ACTCCAAGAC CCAGTGTGCC

6451 CTAAGACACC AGCACTCAGG AGATTGTGAG ACTCCCTGAT CCCTGCACCA

AloI
AloI
6501 CTCTGAGACC AGAAACTAGA ACTTTTATTC CTCATGCTCC TGAAATAGAT

6551 GTCTTGGCAT TTAGTACATT CTTTTCCTTG CACTCCCAAC CCAGAATCCA

AfeI
Bpu10I
6601 GCTCCACAGA TACATTGCTA CTGTCATCAT AAAAAGATCC TGAGCGCTGC

Tth111I
6651 CTTATTCTGG GTTTGGCAGT GGAGTGCTGC CAGACACAGT CGATCGGGAC

6701 CTAGAACCTT GGTTAGGCAT AAAGAAGCAG GATGTGATAG AAGAAGTATT

6751 TAATGGTGGA ACGTTGAGAC TGTCTGCAG ACAAGGGTGG AAGGCTCTGG

NcoI
6801 CTGAACAGCG TTGGGAGGCA ATTCTCCATG GTTCTGTAC GATCTGTGT

Fig. 21A-7

5951 GTCTTCTGAG CAAAGACAGC AACACCTTTT TTTTCTGGA TTGTTGTTTC

EcoRV

6901 AAGGATGTTT GTAAAGCAGG CATCCTTGCA AGATGATATC TCTCTCAGAT

6951 CCAGGCTTGC TTACTGTCCT AGATAATAAA GATAATGTCT CTTACAACAG

7001 ATTTGTTTAC TGTCAAGGAC AATCAATACA ATATGTTTCT CCAGAGTAGG

7051 TCTGTTTTCA ATCCAAGATC ATGAAGATAA TATCTTCATC AGAGACAAAG

7101 GCTGAGCAGG TTGCAAGTT GTCCCAGTAT AAGATTGAGG ATTCCTAATC

7151 TCAGGTTTCT CACCAAGTGGC ACAAACCCCG TGTGCACAGC ATCCACCTAG

NeoI

BstEII

7201 ACTGCTCTGG TCACCATGGT TCTGTCACGT ATCTGTGTGT CTTCTGAGCA

7251 AAGACAGCAA CACCTTTTTT TCTGGATTGT TGTTTCAAGG ATGTTGTAAA

EcoRV

7301 GCAGGCATCC TTGCAAGATG ATATCTCTCT CAGATCCAGG CTTGCTTACT

7351 GTCCTAGATA ATAAAGATAA TGTCTCTTAC AACAGATTG TTTACTGTCA

7401 AGGACAATCA ATACAATATG TTCCTCCAGA GTAGGTCTGT TTTCAATCCA

7451 AGATCATGAA GATAATATCT TCATCAGAGA CAAAGGCTGA GCAGGTTTGC

7501 AAGTTGTCCC AGTATAAGAT TGAGGATTCC TAATCTCAGG TTTCTCACCA

BstEII

7551 GTGGCACAAA CCCCCTGTGC ACAGCATCCA CCTAGACTGC TCTGGTCACC

7601 CTACAAGATT TGGGGGGGGC AAGGTGTACT AATGTGAACA TGAACCTCAT

7651 GCTGTCTGCT AAGCTGTGAG CAGTAAAAGC CTTTGCCTCT GACTCAGGAG

7701 TCTCATGGAC TCTGCCAGCA TTCACAAAAC TCTGGAAAGT TAGCTTATTT

7751 GTTTGCAAGT CAGTAAAATG TCAGCCCCTT CAGAGTTACT GACAAACAGG

MscI PvuII

SanDI

7801 TGGGCACTGA GACTGCACTG GCCAGCTGGG AATAGAGATA GGAGGGGACC

PvuII

7851 CAGCTGGATG CAGTGGGCAG TGGGGGTCAT AGAGTCAAGA GGGTACAGAA

7901 TACAATGGGG TCCTAGTATC ATGGTGGAGG TCAGAAAGAG CCCTAAAAGA

7951 GAGGGTCAAG GTAGGAGGTT AGTGAAGGTC CACCTCCACC CTCTCCAGGA

AseI

8001 CAGGGACATC AGGCCACAAT TAATTTCTCT GCAGTTGGTG AGTGGTCATG

Fig. 21A-8

8051 GTCTCTGGAG TCCCCAGCAT CCAGAGTGTC CCTGGTCTAG TGGTCCCCCC
8101 TTTCTGAGCC ACAGCCACTT TCTCCATCAA ATGAGGCCAG TAATACCCAT
8151 CCCATAGTGA TGCTGTGAGG ATGAGATGAG CATCTGTAAG TGCTGAAGAT
8201 AATCCCTGAC ACATCCCAAG CATTGAGCAG TGCAAGCATA CACTTACACG
8251 GCACTCCCCA GAGCCAGGCA TGTGCTGGTG CCTCATAACAC GTGACCACAT
8301 TTGATCGTCA CAATGACCCT GTGAGGGAGA CTGTGCAACA GAGGACTGAC
8351 CTTGCTCAAA GACCTCAGGC GTTTCCCCTC AGAGCCTGAG AGGTCATCTC
8401 TTTTTTTTTT TTTTTTTCCT TTCTTTCTTT TTCTTTTCCA TTTCTTTTTC
8451 TTTGCAAGAG GTCATCTCTA ATGCTTTGGA ATATCCTGCC AGATTAGAGT
8501 CCCTTTGTTC ACCTGAAGGT TTGGGCCACA CCAGATAGTC TAACGGTGTG
8551 ATTTGTGCTG AAGGTTTTGA GCCACACTAT ATCAGCTAGA TTTCTAGAGC
8601 GGCCGGCCGC AATAAAATAT CTTTATTTTC ATTACATCTG TGTGTTGGTT
8651 TTTTGTGTGA ATCGATAGTA CTAACATACG CTCTCCATCA AAACAAAACG
8701 AAACAAAACA AACTAGCAAA ATAGGCTGTC CCCAGTGCAA GTGCAGGTGC
8751 CAGAACATTT CTCTATCGAT A

ORIGINAL TSTA (aka Pbcvp2g5 -L)

Legend: G5 DNA BINDING SITES -(Magenta)
 E4TATA PROMOTER -(Red)
 LUCIFERASE+ CODING REGION -(Blue)
 VP2 (DUPLICATED VP16 ACTIVATION DOMAIN) -(Aqua)
 GAL4 DNA BINDING DOMAIN -(Green)
 PSA PROXIMAL PROMOTER -(Purple)
 PSA ENHANCER CORES (DUPLICATED)-(Yellow)

KpnI
 Acc65I HindIII SbfI
 1 GGTACCGAGC TCATTTAGGT GACACTATAG AATACAAGCT TGCATGCCTG
 CCATGGCTCG AGTAAATCCA CTGTGATATC TTATGTTTGA ACGTACGGAC
 51 CAGGTCCGGA GGACAGTACT CCGCTCGGAG GACAGTACTC CGCTCGGAGG
 GTCCAGGCCT CCTGTCATGA GCGGAGCCTC CTGTCATGAG GCGAGCCTCC
 101 ACAGTACTCC GCTCGGAGGA CAGTACTCCG CTCGGAGGAC AGTACTCCGA
 TGTTCATGAGG CGAGCCTCCT GTCATGAGGC GAGCCTCCTG TCATGAGGCT
 XbaI BamHI
 151 CTCTAGAGGA TCCCCAGTCC TATATATACT CGCTCTGCAC TTGGCCCTTT
 GAGATCTCCT AGGGGTCAGG ATATATATGA GCGAGACGTG AACCGGGAAA
 BglII
 XhoI
 201 TTTACACTGT GACTGATTGA GCTGGTGCCG TGTCGAGTGG TGTCTCGAGA
 AAATGTGACA CTGACTAACT CGACCACGGC ACAGCTCACC ACAGAGCTCT
 HindIII NcoI
 251 TCTGCGATCT AAGTAAGCTT GGCATTCCGG TACTGTTGGT AAAGCCACCA
 AGACGCTAGA TTCATTGAA CCGTAAGGCC ATGACAACCA TTTCGGTGGT
 M Frame 3
 SfoI
 NarI
 KsiI
 BbeI
 301 TGGAAGACGC CAAAAACATA AAGAAAGGCC CGGCGCCATT CTATCCGCTG
 ACCTTCTGCG GTTTTTGTAT TTCTTTCCGG GCCGCGGTAA GATAGGCGAC
 E D A K N I K K G P A P F Y P L Frame 3
 351 GAAGATGGAA CCGCTGGAGA GCAACTGCAT AAGGCTATGA AGAGATACGC
 CTTCTACCTT GGCGACCTCT CGTTGACGTA TTCCGATACT TCTCTATGCG
 E D G T A G E Q L H K A M K R Y A Frame 3
 401 CCTGGTTCCT GGAACAATTG CTTTTACAGA TGCACATATC GAGGTGGACA
 GGACCAAGGA CTTGTGTAAC GAAAATGTCT ACGTGTATAG CTCCACCTGT
 L V P G T I A F T D A H I E V D I Frame 3

Fig. 21B-1

BstBI

451 TCACITACGC TGAGTACTTC GAAATGTCCG TTCGGTTGGC AGAAGCTATG
 AGTGAATGCG ACTCATGAAG CTTTACAGGC AAGCCAACCG TCTTCGATAC
 T Y A E Y F E M S V R L A E A M Frame 3

501 AAACGATATG GGCTGAATAC AAATCACAGA ATCGTCGTAT GCAGTGAAAA
 TTTGCTATAC CCGACTTATG TTTAGTGTCT TAGCAGCATA CGTCACTTTT
 K R Y G L N T N H R I V V C S E N Frame 3

551 CTCTCTTCAA TTCTTTATGC CGGTGTTGGG CGCGTTATTT ATCGGAGTTG
 GAGAGAAGTT AAGAAATACG GCCACAACCC GCGCAATAAA TAGCCTCAAC
 S L Q F F M P V L G A L F I G V A Frame 3

601 CAGTTGCGCC CGCGAACGAC ATTTATAATG AACGTGAATT GCTCAACAGT
 GTCAACGCGG GCGCTTGCTG TAAATATTAC TTGCACTTAA CGAGTTGTCA
 V A P A N D I Y N E R E L L N S Frame 3

651 ATGGGCATTT CGCAGCCTAC CGTGGTGTTT GTTTCCAAAA AGGGGTTGCA
 TACCCGTAAA GCGTCGGATG GCACCACAAG CAAAGGTTTT TCCCCAACGT
 M G I S Q P T V V F V S K K G L Q Frame 3

701 AAAAATTTTG AACGTGCAAA AAAAGCTCCC AATCATCCAA AAAATTATTA
 TTTTAAAC TTGCACGTTT TTTTCGAGGG TTAGTAGGTT TTTTAATAAT
 K I L N V Q K K L P I I Q K I I I Frame 3

BsrGI

751 TCATGGATTC TAAACGGAT TACCAGGGAT TTCAGTCGAT GTACACGTTT
 AGTACCTAAG ATTTTGCCTA ATGGTCCCTA AAGTCAGCTA CATGTGCAAG
 M D S K T D Y Q G F Q S M Y T F Frame 3

801 GTCACATCTC ATCTACCTCC CGGTTTTAAT GAATACGATT TTGTGCCAGA
 CAGTGTAGAG TAGATGGAGG GCCAAAATTA CTTATGCTAA AACACGGTCT
 V T S H L P P G F N E Y D F V P E Frame 3

BclI

851 GTCCTTCGAT AGGGACAAGA CAATTGCACT GATCATGAAC TCCTCTGGAT
 CAGGAAGCTA TCCCTGTTCT GTTAACGTGA CTAGTACTTG AGGAGACCTA
 S F D R D K T I A L I M N S S G S Frame 3

901 CTA CTGCTCTG GCCTAAAGGT GTCGCTCTGC CTCATAGAAC TGCCTGCGTG
 GATGACCAGA CGGATTTCAC CAGCGAGACG GAGTATCTTG ACGGACGCAC
 T G L P K G V A L P H R T A C V Frame 3

951 AGATTCTCGC ATGCCAGAGA TCCTATTTTT GGCAATCAAA TCATTCCGGA
 TCTAAGAGCG TACGGTCTCT AGGATAAAAA CCGTTAGTTT AGTAAGGCCT
 R F S H A R D P I F G N Q I I P D Frame 3

1001 TACTGCGATT TTAAGTGTG TTCCATTCCA TCACGGTTTT GGAATGTTTA
 ATGACGCTAA AATTCACAAC AAGGTAAGGT AGTGCCAAAA CTTACAAAT
 T A I L S V V P F H H G F G M F T Frame 3

1051 CTACACTCGG ATATTTGATA TGTGGATTTC GAGTCGTCTT AATGTATAGA
 GATGTGAGCC TATAAACTAT ACACCTAAAG CTCAGCAGAA TTACATATCT
 T L G Y L I C G F R V V L M Y R Frame 3

SapI

1101 TTTGAAGAAG AGCTGTTTCT GAGGAGCCTT CAGGATTACA AGATTCAAAG

Fig. 21B-2

	AAACTTCTTC	TCGACAAAGA	CTCCTCGGAA	GTCCTAATGT	TCTAAGTTTC	
	F E E E	L F L	R S L	Q D Y K	I Q S	Frame 3
1151	TGCGCTGCTG	GTGCCAACCC	TATTCTCCTT	CTTCGCCAAA	AGCACTCTGA	
	ACGCGACGAC	CACGGTTGGG	ATAAGAGGAA	GAAGCGGTTT	TCGTGAGACT	
	A L L	V P T L	F S F	F A K	S T L I	Frame 3
1201	TTGAÇAAATA	CGATTTATCT	AATTTACACG	AAATTGCTTC	TGGTGGCGCT	
	AACTGTTTTAT	GCTAAATAGA	TTAAATGTGC	TTTAACGAAG	ACCACCGCGA	
	D K Y	D L S	N L H E	I A S	G G A	Frame 3
1251	CCCCTCTCTA	AGGAAGTCGG	GGAAGCGGTT	GCCAAGAGGT	TCCATCTGCC	
	GGGGAGAGAT	TCCTTCAGCC	CCTTCGCCAA	CGGTTCTCCA	AGGTAGACGG	
	P L S K	E V G	E A V	A K R F	H L P	Frame 3
1301	AGGTATCAGG	CAAGGATATG	GGCTCACTGA	GACTACATCA	GCTATTCTGA	
	TCCATAGTCC	GTTCCTATAC	CCGAGTGA CT	GATGTAGT	CGATAAGACT	
	G I R	Q G Y G	L T E	T T S	A I L I	Frame 3
1351	TTACACCCGA	GGGGGATGAT	AAACCGGGCG	CGGTCGGTAA	AGTTGTTCCA	
	AATGTGGGCT	CCCCTACTA	TTTGGCCCCG	GCCAGCCATT	TCAACAAGGT	
	T P E	G D D	K P G A	V G K	V V P	Frame 3
1401	TTTTTTGAAG	CGAAGGTTGT	GGATCTGGAT	ACCGGGAAAA	CGCTGGGCGT	
	AAAAAACTTC	GCTTCCAACA	CCTAGACCTA	TGGCCCTTTT	GCGACCCGCA	
	F F E A	K V V	D L D	T G K T	L G V	Frame 3
1451	TAATCAAAGA	GGCGAACTGT	GTGTGAGAGG	TCCTATGATT	ATGTCCGGTT	
	ATTAGTTTCT	CCGCTTGACA	CACACTCTCC	AGGATACTAA	TACAGGCCAA	
	N Q R	G E L C	V R G	P M I	M S G Y	Frame 3
1501	ATGTAAACAA	TCCGGAAGCG	ACCAACGCCT	TGATTGACAA	GGATGGATGG	
	TACATTTGTT	AGGCCTTCGC	TGGTTGCGGA	ACTAACTGTT	CCTACCTACC	
	V N N	P E A	T N A L	I D K	D G W	Frame 3
1551	CTACATTCTG	GAGACATAGC	TTACTGGGAC	GAAGACGAAC	ACTTCTTCAT	
	GATGTAAGAC	CTCTGTATCG	AATGACCCTG	CTTCTGCTTG	TGAAGAAGTA	
	L H S G	D I A	Y W D	E D E H	F F I	Frame 3
1601	CGTTGACCGC	CTGAAGTCTC	TGATTAAGTA	CAAAGGCTAT	CAGGTGGCTC	
	GCAACTGGCG	GACTTCAGAG	ACTAATTCAT	GTTTCCGATA	GTCCACCGAG	
	V D R	L K S L	I K Y	K G Y	Q V A P	Frame 3
1651	CCGCTGAATT	GGAATCCATC	TTGCTCCAAC	ACCCCAACAT	CTTCGACGCA	
	GGCGACTTAA	CCTTAGGTAG	AACGAGGTTG	TGGGGTTGTA	GAAGCTGCGT	
	A E L	E S I	L L Q H	P N I	F D A	Frame 3
	SgrAI					
1701	GGTGTGCGAG	GTCTTCCCGA	CGATGACGCC	GGTGAAC TTC	CCGCCGCCGT	
	CCACAGCGTC	CAGAAGGGCT	GCTACTCCGG	CCACTTGAAG	GGCGGCGGCA	
	G V A G	L P D	D D A	G E L P	A A V	Frame 3
1751	TGTTGTTTTG	GAGCACGGAA	AGACGATGAC	GGAAAAAGAG	ATCGTGGATT	
	ACAACAAAAC	CTCGTGCCTT	TCTGCTACTG	CCTTTTCTC	TAGCACCTAA	
	V V L	E H G K	T M T	E K E	I V D Y	Frame 3
1801	ACGTCGCCAG	TCAAGTAACA	ACCGCGAAAA	AGTTGCGCGG	AGGAGTTCTG	

Fig. 21B-3

	TGCAGCGGTC	AGTTCATTGT	TGGCGCTTTT	TCAACGCGCC	TCCTCAACAC	
	V A S	Q V T	T A K K	L R G	G V V	Frame 3
1851	TTTGTGGACG	AAGTACCGAA	AGGTCTTACC	GGAAAACTCG	ACGCAAGAAA	
	AAACACCTGC	TTCATGGCTT	TCCAGAATGG	CCTTTTGAGC	TGCGTTCTTT	
	F V D E	V P K	G L T	G K L D	A R K	Frame 3
1901	AATCAGAGAG	ATCCTCATAA	AGGCCAAGAA	GGGCGGAAAG	ATCGCCGTGT	
	TTAGTCTCTC	TAGGAGTATT	TCCGTTCTT	CCCGCCTTTC	TAGCGGCACA	
	I R E	I L I K	A K K	G G K	I A V *	Frame 3
	XbaI	FseI				
1951	AATTCTAGAG	TCGGGGCGGC	CGGCCGCTTC	GAGCAGACAT	GATAAGATAC	
	TTAAGATCTC	AGCCCCGCCG	GCCGGCGAAG	CTCGTCTGTA	CTATTCTATG	
2001	ATTGATGAGT	TTGGACAAAC	CACAACTAGA	ATGCAGTGAA	AAAAATGCTT	
	TAACTACTCA	AACCTGTTTG	GTGTTGATCT	TACGTCACCT	TTTTTACGAA	
2051	TATTTGTGAA	ATTTGTGATG	CTATTGCTTT	ATTTGTAACC	ATTATAAGCT	
	ATAAACACTT	TAAACACTAC	GATAACGAAA	TAAACATTGG	TAATATTCTGA	
2101	GCAATAAACA	AGTTAACAAC	AACAATTGCA	TTCATTTTAT	GTTTCAGGTT	
	CGTTATTTGT	TCAATTGTTG	TTGTTAACGT	AAGTAAAATA	CAAAGTCCAA	
2151	CAGGGGGAGG	TGTGGGAGGT	TTTTTAAAGC	AAGTAAAACC	TCTACAAATG	
	GTCCCCCTCC	ACACCCCTCC	AAAAATTTTC	TTCATTTTGG	AGATGTTTAC	
		BamHI	SalI			
2201	TGGTAAAATC	GATAAGGATC	CGTCGACCGA	TGCCCTTGAG	AGCCTTCAAC	
	ACCATTTTAG	CTATTCCTAG	GCAGCTGCCT	ACGGGAACCTC	TCGGAAGTTG	
2251	CCAGTCAGCT	CCTTCCGGTG	GGCGCGGGGC	ATGACTATCG	TCGCCGCACT	
	GGTCAGTCGA	GGAAGGCCAC	CCGCGCCCCG	TACTGATAGC	AGCGGCGTGA	
				SapI		
2301	TATGACTGTC	TTCTTTATCA	TGCAACTCGT	AGGACAGGTG	CCGGCAGCGC	
	ATACTGACAG	AAGAAATAGT	ACGTTGAGCA	TCCTGTCCAC	GGCCGTGCGG	
2351	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	CGCTCGGTG	TTCGGCTGCG	
	AGAAGGCGAA	GGAGCGAGTG	ACTGAGCGAC	GCGAGCCAGC	AAGCCGACGC	
2401	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	TCCACAGAAT	
	CGCTCGCCAT	AGTCGAGTGA	GTTTCCGCCA	TTATGCCAAT	AGGTGTCTTA	
2451	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	
	GTCCCCTATT	GCGTCCTTTC	TTGTACACTC	GTTTCCGGT	CGTTTCCGGG	
2501	AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	
	TCCTTGGCAT	TTTTCCGGCG	CAACGACCGC	AAAAAGGTAT	CCGAGGCGGG	
2551	CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	
	GGGACTGCTC	GTAGTGTTTT	TAGCTGCGAG	TTCAGTCTCC	ACCGCTTTGG	
				BssSI		
2601	CGACAGGACT	ATAAAGATAC	CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	

Fig. 21B-4

	GCTGTCCTGA	TATTTCTATG	GTCCGCAAAG	GGGGACCTTC	GAGGGAGCAC	
2651	CGCTCTCCTG	TTCCGACCTT	GCCGCTTACC	GGATACCTGT	CCGCCTTTCT	
	GCGAGAGGAC	AAGGCTGGGA	CGGCGAATGG	CCTATGGACA	GGCGGAAAGA	
2701	CCCTTCGGGA	AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	
	GGGAAGCCCT	TCGCACCGCG	AAAGAGTTAC	GAGTGCGACA	TCCATAGAGT	
2751	GTTCCGGTGTA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	
	CAAGCCACAT	CCAGCAAGCG	AGGTTTCGACC	CGACACACGT	GCTTGGGGGG	
2801	GTTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	TTGAGTCCAA	
	CAAGTCGGGC	TGGCGACGCG	GAATAGGCCA	TTGATAGCAG	AACTCAGGTT	
2851	CCCGGTAAGA	CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	
	GGGCCATTCT	GTGCTGAATA	GCGGTGACCG	TCGTCGGTGA	CCATTGTCCT	
2901	TTAGCAGAGC	GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	
	AATCGTCTCG	CTCCATACAT	CCGCCACGAT	GTCTCAAGAA	CTTCACCACC	
2951	CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	GCGCTCTGCT	
	GGATTGATGC	CGATGTGATC	TTCCTGTCAT	AAACCATAGA	CGCGAGACGA	
3001	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	TCCGGCAAAC	
	CTTCGGTCAA	TGGAAGCCTT	TTTCTCAACC	ATCGAGAACT	AGGCCGTTTG	
3051	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	
	TTTGGTGGCG	ACCATCGCCA	CCAAAAAAC	AAACGTTTCG	CGTCTAATGC	
3101	CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	
	GCGTCTTTTT	TTCTTAGAGT	TCTTCTAGGA	AACTAGAAAA	GATGCCCCAG	
3151	TGACGCTCAG	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	
	ACTGCGAGTC	ACCTTGCTTT	TGAGTGCAAT	TCCCTAAAC	CAGTACTCTA	
3201	TATCAAAAAG	GATCTTCACC	TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	
	ATAGTTTTTC	CTAGAAGTGG	ATCTAGGAAA	ATTTAATTTT	TACTTCAAAA	
3251	AAATCAATCT	AAAGTATATA	TGAGTAAACT	TGGTCTGACA	GTTACCAATG	
	TTTAGTTAGA	TTTCATATAT	ACTCATTTGA	ACCAGACTGT	CAATGGTTAC	
				* W H	Frame 4	
3301	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	CGTTCATCCA	
	GAATTAGTCA	CTCCGTGGAT	AGAGTCGCTA	GACAGATAAA	GCAAGTAGGT	
	K I L	S A G	I E A I	Q R N	R E D	Frame 4
	AhdI					
3351	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	
	ATCAACGGAC	TGAGGGGCAG	CACATCTATT	GATGCTATGC	CCTCCCGAAT	
	M T A Q	S G T	T Y I	V V I R	S P K	Frame 4
3401	CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC	
	GGTAGACCGG	GGTCACGACG	TTACTATGGC	GCTCTGGGTG	CGAGTGGCCG	
	G D P	G L A A	I I G	R S G	R E G A	Frame 4
	BglI					
3451	TCCAGATTTA	TCAGCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	

Fig. 21B-5

	AGGTCTAAAT	AGTCGTTATT	TGGTCGGTCG	GCCTTCCCGG	CTCGCGTCTT	
	C S K	D A I	F W G A	P L A	S R L	Frame 4
	AseI					
3501	GTGGTCCTGC	AACTTTATCC	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	
	CACCAGGACG	TTGAAATAGG	CGGAGGTAGG	TCAGATAATT	AACAACGGCC	
	L P G A	V K D	A E M	W D I L	Q Q R	Frame 4
	FspI					
3551	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	AGTTTGCGCA	ACGTTGTTGC	
	CTTCGATCTC	ATTCATCAAG	CGGTCAATTA	TCAAACGCGT	TGCAACAACG	
	S A L	T L L E	G T L	L K R	L T T A	Frame 4
3601	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	ATGGCTTCAT	
	GTAACGATGT	CCGTAGCACC	ACAGTGCAGG	CAGCAAACCA	TACCGAAGTA	
	M A V	P M T	T D R E	D N P	I A E	Frame 4
3651	TCAGCTCCGG	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	
	AGTCGAGGCC	AAGGGTTGCT	AGTTCGCGTC	AATGTACTAG	GGGGTACAAC	
	N L E P	E W R	D L R	T V H D	G M N	Frame 4
3701	TGCAAAAAAG	CGGTTAGCTC	CTTCGGTCCT	CCGATCGTTG	TCAGAAGTAA	
	ACGTTTTTTC	GCCAATCGAG	GAAGCCAGGA	GGCTAGCAAC	AGTCTTCATT	
	H L F	A T L E	K P G	G I T	T L L L	Frame 4
3751	GTTGGCCGCA	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	
	CAACCGGCGT	CACAATAGTG	AGTACCAATA	CCGTCGTGAC	GTATTAAGAG	
	N A A	T N D	S M T I	A A S	C L E	Frame 4
3801	TTACTGTCAT	GCCATCCGTA	AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	
	AATGACAGTA	CGGTAGGCAT	TCTACGAAAA	GACACTGACC	ACTCATGAGT	
	R V T M	G D T	L H K	E T V P	S Y E	Frame 4
3851	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC	
	TGGTTCAGTA	AGACTCTTAT	CACATACGCC	GCTGGCTCAA	CGAGAACGGG	
	V L D	N Q S Y	H I R	R G L	Q E Q G	Frame 4
3901	GGCGTCAATA	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC	
	CCGCAGTTAT	GCCCTATTAT	GGCGCGGTGT	ATCGTCTTGA	AATTTTCACG	
	A D I	R S L	V A G C	L L V	K F T	Frame 4
	XmnI					
3951	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	
	AGTAGTAACC	TTTTGCAAGA	AGCCCCGCTT	TTGAGAGTTC	CTAGAATGGC	
	S M M P	F R E	E P R	F S E L	I K G	Frame 4
	BssSI					
4001	CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGACCCCA	ACTGATCTTC	
	GACAACTCTA	GGTCAAGCTA	CATTGGGTGA	GCACGTGGGT	TGACTAGAAG	
	S N L	D L E I	Y G V	R A G	L Q D E	Frame 4
4051	AGCATCTTTT	ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	
	TCGTAGAAAA	TGAAAGTGGT	CGCAAAGACC	CACCTCGTTTT	TGTCCTTCCG	
	A D K	V K V	L T E P	H A F	V P L	Frame 4
4101	AAAATGCCGC	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	
	TTTTACGGCG	TTTTTTCCTT	TATTCCTCGT	GTGCCTTTAC	AACTTATGAG	

Fig. 21B-6

C F A A F F P I L A V R F H Q I S Frame 4

4151 A T A C T C T T C C T T T T T C A A T A T T A T T G A A G C A T T T A T C A G G G T T A T T G T C T
T A T G A G A A G G A A A A A G T T A T A A T A A C T T C G T A A A T A G T C C C A A T A A C A G A
M F r a m e 4

4201 C A T G A G C G G A T A C A T A T T T G A A T G T A T T T A G A A A A A T A A A C A A A T A G G G G
G T A C T C G C C T A T G T A T A A A C T T A C A T A A A T C T T T T T A T T T G T T T A T C C C C

4251 T T C C G C G C A C A T T T C C C C G A A A A G T G C C A C C T G A C G C G C C C T G T A G C G G C
A A G G C G C G T G T A A A G G G G C T T T C A C G G T G G A C T G C G C G G G A C A T C G C C G

4301 G C A T T A A G C G C G G C G G G T G T G G T G G T T A C G C G C A G C G T G A C C G C T A C A C T
C G T A A T T C G C G C C G C C C A C A C C A C C A A T G C G C G T C G C A C T G G C G A T G T G A

4351 T G C C A G C G C C C T A G C G C C C G C T C C T T T C G C T T T C T T C C C T T C C T T T C T C G
A C G G T C G C G G G A T C G C G G G C G A G G A A A G C G A A A G A A G G G A A G G A A A G A G C

4401 C C A C G T T C G C C G G C T T T C C C C G T C A A G C T C T A A A T C G G G G G C T C C C T T T A
G G T G C A A G C G G C C G A A A G G G G C A G T T C G A G A T T T A G C C C C C G A G G G A A A T

4451 G G G T T C C G A T T T A G T G C T T T A C G G C A C C T C G A C C C C A A A A A A C T T G A T T A
C C C A A G G C T A A A T C A C G A A T G C C G T G G A G C T G G G G T T T T T T G A A C T A A T

D r a I I I

4501 G G G T G A T G G T T C A C G T A G T G G G C C A T C G C C C T G A T A G A C G G T T T T T C G C C
C C C A C T A C C A A G T G C A T C A C C C G G T A G C G G G A C T A T C T G C C A A A A A G C G G

A l o I
A l o I

4551 C T T T G A C G T T G G A G T C C A C G T T C T T T A A T A G T G G A C T C T T G T T C C A A A C T
G A A A C T G C A A C C T C A G G T G C A A G A A A T T A T C A C C T G A G A A C A A G G T T T G A

4601 G G A A C A A C A C T C A A C C C T A T C T C G G T C T A T T C T T T T G A T T T A T A A G G G A T
C C T T G T T G T G A G T T G G G A T A G A G C C A G A T A A G A A A A C T A A A T A T T C C C T A

4651 T T T G C C G A T T T C G G C C T A T T G G T T A A A A A A T G A G C T G A T T T A A C A A A A A T
A A A C G G C T A A A G C C G G A T A A C C A A T T T T T T A C T C G A C T A A A T T G T T T T T A

B g l I

4701 T T A A C G C G A A T T T T A A C A A A A T A T T A A C G T T T A C A A T T T C C C A T T C G C C A
A A T T G C G C T T A A A A T T G T T T T A T A A T T G C A A A T G T T A A A G G G T A A G C G G T

F s p I

4751 T T C A G G C T G C G C A A C T G T T G G G A A G G G C G A T C G G T G C G G G C C T C T T C G C T
A A G T C C G A C G C G T T G A C A A C C C T T C C G C T A G C C A C G C C C G G A G A A G C G A

4801 A T T A C G C C A G C C C A A G C T A C C A T G A T A A G T A A G T A A T A T T A A G G T A C G G G
T A A T G C G G T C G G G T T C G A T G G T A C T A T T C A T T C A T T A T A A T T C C A T G C C C

N o t I

4851 A G G T A C T T G G A G C G G C C G C G A T C C A G A C A T G A T A A G A T A C A T T G A T G A G T
T C C A T G A A C C T C G C C G G C G C T A G G T C T G T A C T A T T C T A T G T A A C T A C T C A

4901 T T G G A C A A A C C A C A A C T A G A A T G C A G T G A A A A A A T G C T T T A T T T G T G A A
A A C C T G T T T G G T G T T G A T C T T A C G T C A C T T T T T T T A C G A A A T A A A C A C T T

Fig. 21B-7

4951 ATTTGTGATG CTATTGCTTT ATTTGTAACC ATTATAAGCT GCAATAAACA
TAAACACTAC GATAACGAAA TAAACATTGG TAATATTCTGA CGTTATTTGT

5001 AGTTAACAAC AACAAATTGCA TTCATTTTAT GTTTCAGGTT CAGGGGGAGG
TCAATTGTTG TTGTTAACGT AAGTAAATA CAAAGTCCAA GTCCCCCTCC

5051 TGTGGGAGGT TTTTAAAGC AAGTAAACC TCTACAAATG TGGTATGGCT
ACACCCTCCA AAAAATTTCTG TTCATTTTGG AGATGTTTAC ACCATACCGA

BclI

5101 GATTATGATC ATGAACAGAC TGTGAGGACT GAGGGGCCTG AAATGAGCCT
CTAATACTAG TACTTGTCTG AACTCCTGA CTCCCCGAC TTTACTCGGA

5151 TGGGACTGTG AATTTAAAT ACACAAACAA TTAGAATCAG TAGTTTAAAC
ACCCTGACAC TTAAATTTTA TGTGTTTGT AATCTTAGTC ATCAAATTGT

5201 CATTATACAC TAAAAATTT TATATTTACC TTAGAGCTTT AAATCTCTGT
GTAATATGTG AATTTTAAAT ATATAAATGG AATCTCGAAA TTTAGAGACA

5251 AGGTAGTTTG TCCAATTATG TCACACCACA GAAGTAAGGT TCCTTCACAA
TCCATCAAAC AGGTTAATAC AGTGTGGTGT CTTCAATCCA AGGAAGTGT
* L

Frame 6

SalI

AccI

XbaI

5301 AGATCCCAG CTGTCGACAT TTCTAGAGGA TCTCGGACCC GGGGAATCCC
TCTAGGGTTC GACAGCTGTA AAGATCTCCT AGAGCCTGGG CCCCTTAGGG
S G L S D V N R S S R P G P S D

Frame 6

5351 CGTCCCCCAA CATGTCCAGA TCGAAATCGT CTAGCGCGTC GGCATGCGCC
GCAGGGGGTT GTACAGGTCT AGCTTTAGCA GATCGCGCAG CCGTACGCGG
G D G L M D L D F D D L A D A H A

Frame 6

BtrI

5401 ATCGCCACGT CCTCGCCGTC TAAGTGGAGC TCGTCCCCCA GGCTGACATC
TAGCGGTGCA GGAGCGGCAG ATTCACCTCG AGCAGGGGGT CCGACTGTAG
M A V D E G D L H L E D G L S V D

Frame 6

5451 GGTGGGGGG GCGGATCTCG GACCCGGGGA ATCCCGGTCC CCCAACATGT
CCAGCCCCC CGCCTAGAGC CTGGGCCCCCT TAGGGGCAGG GGGTTGTACA
T P P A S R P G P S D G D G L M

Frame 6

BtrI

5501 CCAGATCGAA ATCGTCTAGC GCGTCGGCAT GCGCCATCGC CACGTCTCTG
GGTCTAGCTT TAGCAGATCG CGCAGCCGTA CGCGGTAGCG GTGCAGGAGC
D L D F D D L A D A H A M A V D E

Frame 6

BamHI

5551 CCGTCTAAGT GGAGCTCGTC CCCCAGGCTG ACATCGGTCTG GGGGGGCGGA
GGCAGATTCA CCTCGAGCAG GGGGTCGAC TGTAGCCAGC CCCCCGCTT
G D L H L E D G L S V D T P P A S

Frame 6

EcoRI

5601 TCCCCCGGGC TGCAGGAATT CCGGCGATAC AGTCAACTGT CTTTGACCTT
AGGGGGCCCCG ACGTCCTTAA GGCCGCTATG TCAGTTGACA GAAACTGGAA
G G P Q L F E P S V T L Q R Q G

Frame 6

Fig. 21B-8

5651 TGTTACTACT CTCTCCGAT GATGATGTCG CACTTATTCT ATGCTGTCTC
 ACAATGATGA GAGAAGGCTA CTACTACAGC GTGAATAAGA TACGACAGAG
 K N S S E E S S S T A S I R H Q R Frame 6

5701 AATGTTAGAG GCATATCAGT CTCCACTGAA GCCAATCTAT CTGTGACGGC
 TTACAATCTC CGTATAGTCA GAGGTGACTT CGGTTAGATA GACACTGCCG
 L T L P M D T E V S A L R D T V A Frame 6

BsrGI

5751 ATCTTTTATTC ACATTATCTT GTACAAATAA TCCTGTTAAC AATGCTTTTA
 TAGAAATAAG TGTAAATAGAA CATGTTTATT AGGACAAATG TTACGAAAT
 D K N V N D Q V F L G T L L A K Frame 6

XhoI

5801 TATCCTGTAA AGAATCCATT TTCAAATCA TGTCAAGGTC TTCTCGAGGA
 ATAGGACATT TCTTAGGTAA AAGTTTTAGT ACAGTTCCAG AAGAGCTCCT
 I D Q L S D M K L I M D L D E R P Frame 6

5851 AAAATCAGTA GAAATAGCTG TTCCAGTCTT TCTAGCCTTG ATTCCACTTC
 TTTTAGTCAT CTTTATCGAC AAGGTCAGAA AGATCGGAAC TAAGGTGAAG
 F I L L F L Q E L R E L R S E V E Frame 6

5901 TGTCAGATGT GCCCTAGTCA GCGGAGACCT TTTGGTTTTG GGAGAGTAGC
 ACAGTCTACA CGGGATCAGT CGCCTCTGGA AAACCAAAAC CCTCTCATCG
 T L H A R T L P S R K T K P S Y Frame 6

5951 GACACTCCCA GTTGTCTTTC AGACACTTGG CGCACTTCGG TTTTCTTTG
 CTGTGAGGGT CAACAAGAAG TCTGTGAACC GCGTGAAGCC AAAAAGAAAC
 R C E W N N K L C K A C K P K E K Frame 6

6001 GAGCACTTGA GCTTTTTAAG TCGGCAAATA TCGCATGCTT GTTCGATAGA
 CTCGTGAACG CGAAAAATTC AGCCGTTTAT AGCGTACGAA CAAGCTATCT
 S C K L K K L R C I D C A Q E I S Frame 6

HindIII

6051 AGACAGTAGC TTCATCTTTC AGGAGGCTTG CTTCAAGCTT GGGGCTGGGG
 TCTGTCTATCG AAGTAGAAAG TCCTCCGAAC GAAGTTCGAA CCCCACCC
 S L L K M Frame 6

6101 AGCCTCCCCC AGGAGCCCTA TAAAACCTTC ATTCCCAGG ACTCCGCCCC
 TCGGAGGGGG TCCTCGGGAT ATTTTGAAG TAAGGGGTCC TGAGGCGGGG

BglI

BstXI

6151 TGCCCTGCTG GCACCCAGAG GCTGACCAAG GCCCTCCCCA TGCTGCTGGA
 ACGGGACGAC CGTGGGTCTC CGACTGGTTC CGGGAGGGGT ACGACGACCT

BstXI

6201 GGCTGGACAA CCCCCTCCCA CACCCAGAGC TGTGGAAGGG GAGGGAGAGC
 CCGACCTGTT GGGGGAGGGT GTGGGTCTCG ACACCTTCCC CTCCCTCTCG

PsrI

PsrI

6251 TAGTACTTGC TGTTCTGCAA TTAGTAGATC ACCCTGGATG CACCAGGCCC
 ATCATGAACG ACAAGACGTT AATGATCTAG TGGGACCTAC GTGGTCCGGG

6301 TGTGGCTCAT GGAGACTTCA TCTAGGGGAC AAAGGCAGAG GAGACACGCC
 ACACCGAGTA CCTCTGAAGT AGATCCCTG TTTCCGTCTC CTCTGTGCGG

Fig. 21B-9

6351 CAGCATGAAA CAGAAACAGG GGGTGGGTAC GATCCCCGAT TCTTCATACA
GTCCTACTTT GTCTTTGTCC CCCACCCATG CTAGGGGGCTA AGAAGTATGT

PmlI

6401 AAGCCTCACG TGCCTAGATC CTTTGCACTC CAAGACCCAG TGTGCCCTAA
TTCGGAGTGC ACGGATCTAG GAAACGTGAG GTTCTGGGTC ACACGGGATT

6451 GACACCAGCA CTCAGGAGAT TGTGAGACTC CCTGATCCCT GCACCACTCT
CTGTGGTCTG GAGTCCTCTA ACACCTCTGAG GGACTAGGGA CGTGGTGAGA

AloI

AloI

6501 GAGACCAGAA ACTAGAACTT TTATTCCTCA TGCTCCTGAA ATAGATGTCT
CTCTGGTCTT TGATCTTGAA AATAAGGAGT ACGAGGACTT TATCTACAGA

6551 TGGCATTTAG TACATTCTTT TCCTTGCACT CCCAACCCAG AATCCAGCTC
ACCGTAAATC ATGTAAGAAA AGGAACGTGA GGGTTGGGTC TTAGGTCGAG

AfeI

Bpu10I

6601 CACAGATACA TTGCTACTGT CATCATAAAA AGATCCTGAG CGCTGCCTTA
GTGTCTATGT AACGATGACA GTAGTATTTT TCTAGGACTC GCGACGGAAT

Tth111I

6651 TTCTGGGTTT GGCAGTGGAG TGCTGCCAGA CACAGTCGAT CGGGACCTAG
AAGACCCAAA CCGTCACCTC ACGACGGTCT GTGTCAGCTA GCCCTGGATC

6701 AACCTTGGTT AGGCATAAAG AAGCAGGATG TGATAGAAGA AGTATTTAAT
TTGGAACCAA TCCGTATTTC TTCGTCTAC ACTATCTTCT TCATAAATTA

6751 GGTGGAACGT TGAGACTGTC CTGCAGACAA GGGTGGAAGG CTCTGGCTGA
CCACCTTGCA ACTCTGACAG GACGTCTGTT CCCACCTTCC GAGACCGACT

NcoI

6801 ACAGCGTTGG GAGGCAATTC TCCATGGTTC TGTCACGTAT CTGTGTGTCT
TGTCGCAACC CTCCGTTAAG AGGTACCAAG ACAGTGCATA GACACACAGA

6851 TCTGAGCAAA GACAGCAACA CCTTTTTTTT TCTGGATTGT TGTTC AAGG
AGACTCGTTT CTGTCGTTGT GGAAAAAAAA AGACCTAACA ACAAAGTTCC

EcoRV

6901 ATGTTTGTAAG AGCAGGCATC CTTGCAAGAT GATATCTCTC TCAGATCCAG
TACAAACATT TCGTCCGTAG GAACGTTCTA CTATAGAGAG AGTCTAGGTC

6951 GCTTGCTTAC TGTCTAGAT AATAAGATA ATGTCTCTTA CAACAGATTT
CGAACGAATG ACAGGATCTA TTATTCTAT TACAGAGAAT GTTGTCTAAA

7001 GTTACTGTC AAGGACAATC AATACAATAT GTTCCTCCAG AGTAGGTCTG
CAAATGACAG TTCCTGTTAG TTATGTTATA CAAGGAGGTC TCATCCAGAC

7051 TTTTCAATCC AAGATCATGA AGATAATATC TTCATCAGAG ACAAAGGCTG
AAAAGTTAGG TTCTAGTACT TCTATTATAG AAGTAGTCTC TGTTCGAC

7101 AGCAGGTTTG CAAGTTGTCC CAGTATAAGA TTGAGGATTC CTAATCTCAG
TCGTCCAAAC GTTCAACAGG GTCATATTCT AACTCCTAAG GATTAGAGTC

Fig. 21B-10

7151 GTTTCTCACC AGTGGCACAA ACCCCGTGTG CACAGCATCC ACCTAGACTG
CAAAGAGTGG TCACCGTGT TGGGGCACAC GTGTCGTAGG TGGATCTGAC

NcoI

BstEII

7201 CTCTGGTCAC CATGGTTCTG TCACGTATCT GTGTGTCTTC TGAGCAAAGA
GAGACCAGTG GTACCAAGAC AGTGCATAGA CACACAGAAG ACTCGTTTCT

7251 CAGCAACACC TTTTTTCTG GATTGTTGTT TCAAGGATGT TGTAAGCAG
GTCGTTGTGG AAAAAAGAC CTAACAACAA AGTTCCTACA ACATTTCGTC

EcoRV

7301 GCATCCTTGC AAGATGATAT CTCTCTCAGA TCCAGGCTTG CTTACTGTCC
CGTAGGAACG TTCTACTATA GAGAGAGTCT AGGTCCGAAC GAATGACAGG

7351 TAGATAATAA AGATAATGTC TCTTACAACA GATTTGTTTA CTGTCAAGGA
ATCTATTATT TCTATTACAG AGAATGTTGT CTAAACAAAT GACAGTTCCT

7401 CAATCAATAC AATATGTTCC TCCAGAGTAG GTCTGTTTTT AATCCAAGAT
GTTAGTTATG TTATAACAAG AGGTCTCATC CAGACAAAAG TTAGGTTCTA

7451 CATGAAGATA ATATCTTCAT CAGAGACAAA GGCTGAGCAG GTTTGCAAGT
GTACTTCTAT TATAGAAGTA GTCTCTGTTT CCGACTCGTC CAAACGTTCA

7501 TGTCCCAGTA TAAGATTGAG GATTCCTAAT CTCAGGTTTC TCACCAGTGG
ACAGGGTCAT ATTCTAACTC CTAAGGATTA GAGTCCAAAG AGTGGTCACC

BstEII

7551 CACAAACCCC GTGTGCACAG CATCCACCTA GACTGCTCTG GTCACCCTAC
GTGTTTGGGG CACACGTGTC GTAGGTGGAT CTGACGAGAC CAGTGGGATG

7601 AAGATTGCGG GGGGGCAAGG TGTACTAATG TGAACATGAA CCTCATGCTG
TTCTAAACCC CCCCCGTTCC ACATGATTAC ACTTGTACTT GGAGTACGAC

7651 TCTGCTAAGC TGTGAGCAGT AAAAGCCTTT GCCTCTGACT CAGGAGTCTC
AGACGATTCG AACTCGTCA TTTTCGGAAA CCGAGACTGA GTCCTCAGAG

7701 ATGGACTCTG CCAGCATTCA CAAACTCTG GAAAGTTAGC TTATTTGTTT
TACCTGAGAC GGTGTAAGT GTTTTGAGAC CTTTCAATCG AATAAACAAA

7751 GCAAGTCAGT AAAATGTCAG CCCCTTCAGA GTTACTGACA AACAGGTGGG
CGTTCAGTCA TTTTACAGTC GGGGAAGTCT CAATGACTGT TTGTCCACCC

PvuII

MscI

SanDI PvuII

7801 CACTGAGACT GCACTGGCCA GCTGGGAATA GAGATAGGAG GGGACCCAGC
GTGACTCTGA CGTGACCGGT CGACCCCTAT CTCTATCCTC CCCTGGGTGC

7851 TGGATGCAGT GGGCAGTGGG GGTCATAGAG TCAAGAGGGT ACAGAATACA
ACCTACGTCA CCCGTCACCC CCAGTATCTC AGTTCTCCCA TGTCTTATGT

7901 ATGGGGTCCCT AGTATCATGG TGGAGGTCAG AAAGAGCCCT AAAAGAGAGG
TACCCAGGA TCATAGTACC ACCTCCAGTC TTTCTCGGGA TTTTCTCTCC

7951 GTCAAGGTAG GAGGTTAGTG AAGGTCCACC TCCACCCTCT CCAGGACAGG
CAGTTCCATC CTCCAATCAC TTCCAGGTGG AGGTGGGAGA GGTCTGTCC

Fig. 21B-11

AseI

8001 GACATCAGGC CACAATTAAT TTCTCTGCAG TTGGTGAGTG GTCATGGTCT
CTGTAGTCCG GTGTTAATTA AAGAGACGTC AACCACTCAC CAGTACCAGA

8051 CTGGAGTCCC CAGCATCCAG AGTGTCCTTG GTCTAGTGGT CCCCCCTTTC
GACCTCAGGG GTCGTAGGTC TCACAGGGAC CAGATCACCA GGGGGGAAAG

8101 TGAGCCACAG CCACTTTCTC CATCAAATGA GGCCAGTAAT ACCCATCCCA
ACTCGGTGTC GGTGAAAGAG GTAGTTTACT CCGGTCATTA TGGGTAGGGT

8151 TAGTGATGCT GTGAGGATGA GATGAGCATC TGTAAGTGCT GAAGATAATC
ATCACTACGA CACTCCTACT CTACTCGTAG ACATTACGA CTTCTATTAG

8201 CCTGACACAT CCAAGCATT CAGCAGTGCA AGCATACTACT TACACGGCAC
GGACTGTGTA GGGTTCGTAA GTCGTCACGT TCGTATGTGA ATGTGCCGTG

PmlI

8251 TCCCCAGAGC CAGGCATGTG CTGGTGCCTC ATACACGTGA CCACATTTGA
AGGGGTCTCG GTCCGTACAC GACCACGGAG TATGTGCACT GGTGTAAACT

8301 TCGTCACAAT GACCCTGTGA GGGAGACTGT GCAACAGAGG ACTGACCTTG
AGCAGTGTTA CTGGGACACT CCCTCTGACA CGTTGTCTCC TGACTGGAAC

Bsu36I

8351 CTCAAAGACC TCAGGCGTTT CCCCTCAGAG CCTGAGAGGT CATCTCTTTT
GAGTTTCTGG AGTCCGCAA GGGGAGTCTC GGACTCTCCA GTAGAGAAAA

8401 TTTTTTTTTT TTTCCTTTCT TTCTTTTCT TTTCCATTTC TTTTCTTTG
AAAAAAAAAA AAAGGAAAGA AAGAAAAAGA AAAGGTAAAG AAAAAGAAAC

8451 CAAGAGGTCA TCTCTAATGC TTTGGAATAT CCTGCCAGAT TAGAGTCCCT
GTTCTCCAGT AGAGATTACG AAACCTTATA GGACGGTCTA ATCTCAGGGA

8501 TTGTTACCTT GAAGGTTTGG GCCACACCAG ATAGTCTAAC GGTGTGATTT
AACAAGTGGA CTTCCAAACC CGGTGTGGTC TATCAGATTG CCACACTAAA

XbaI NotI

8551 GTGCTGAAGG TTTTGAGCCA CACTATATCA GCTAGATTTC TAGAGCGGCC
CACGACTTCC AAAACTCGGT GTGATATAGT CGATCTAAAG ATCTCGCCGG

8601 GCAATAAAAT ATCTTTATTT TCATTACATC TGTGTGTTGG TTTTTGTGT
CGTTATTTTA TAGAAATAAA AGTAATGTAG ACACACAACC AAAAACACA

8651 GAATCGATAG TACTAACATA CGCTCTCCAT CAAAACAAAA CGAAACAAAA
CTTAGCTATC ATGATTGTAT GCGAGAGGTA GTTTTGTTTT GCTTTGTTTT

8701 CAAACTAGCA AAATAGGCTG TCCCCAGTGC AAGTGCAGGT GCCAGAACAT
GTTTGATCGT TTTATCCGAC AGGGGTCACG TTCACGTCCA CGGTCTTGTA

8751 TTCTCTATCG ATA
AAGAGATAGC TAT

Fig. 21B-12

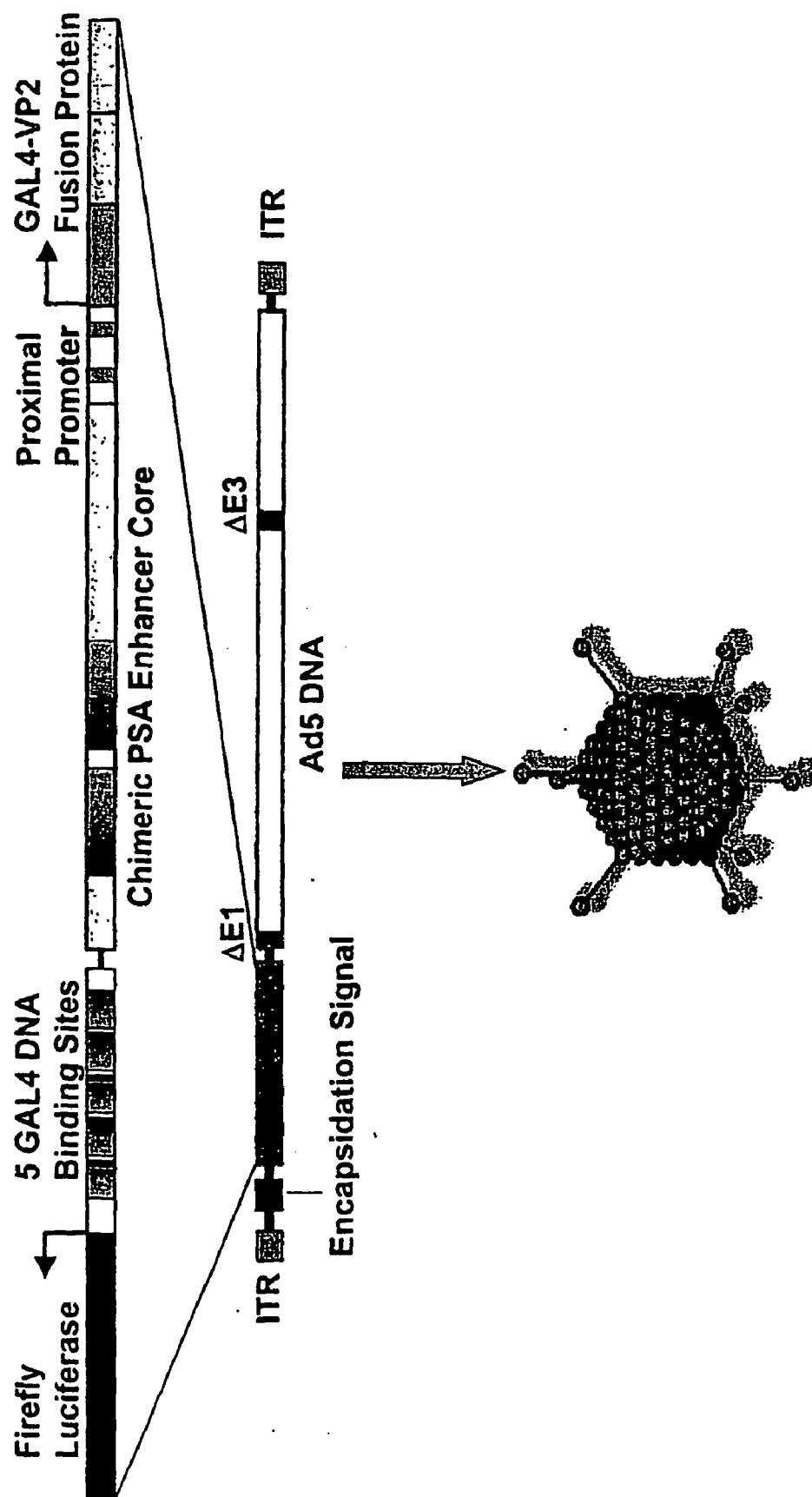


Fig. 22

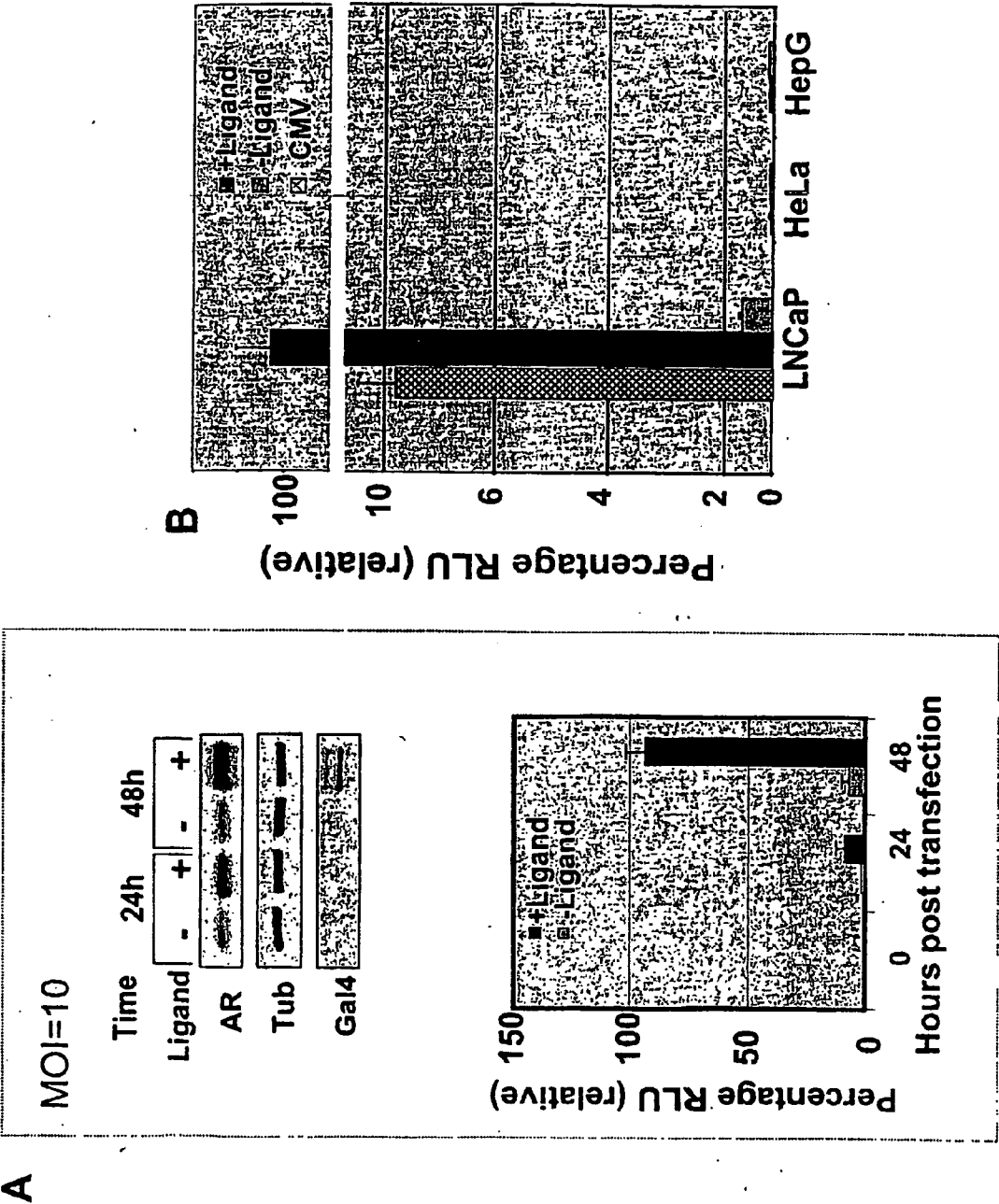


Fig. 23

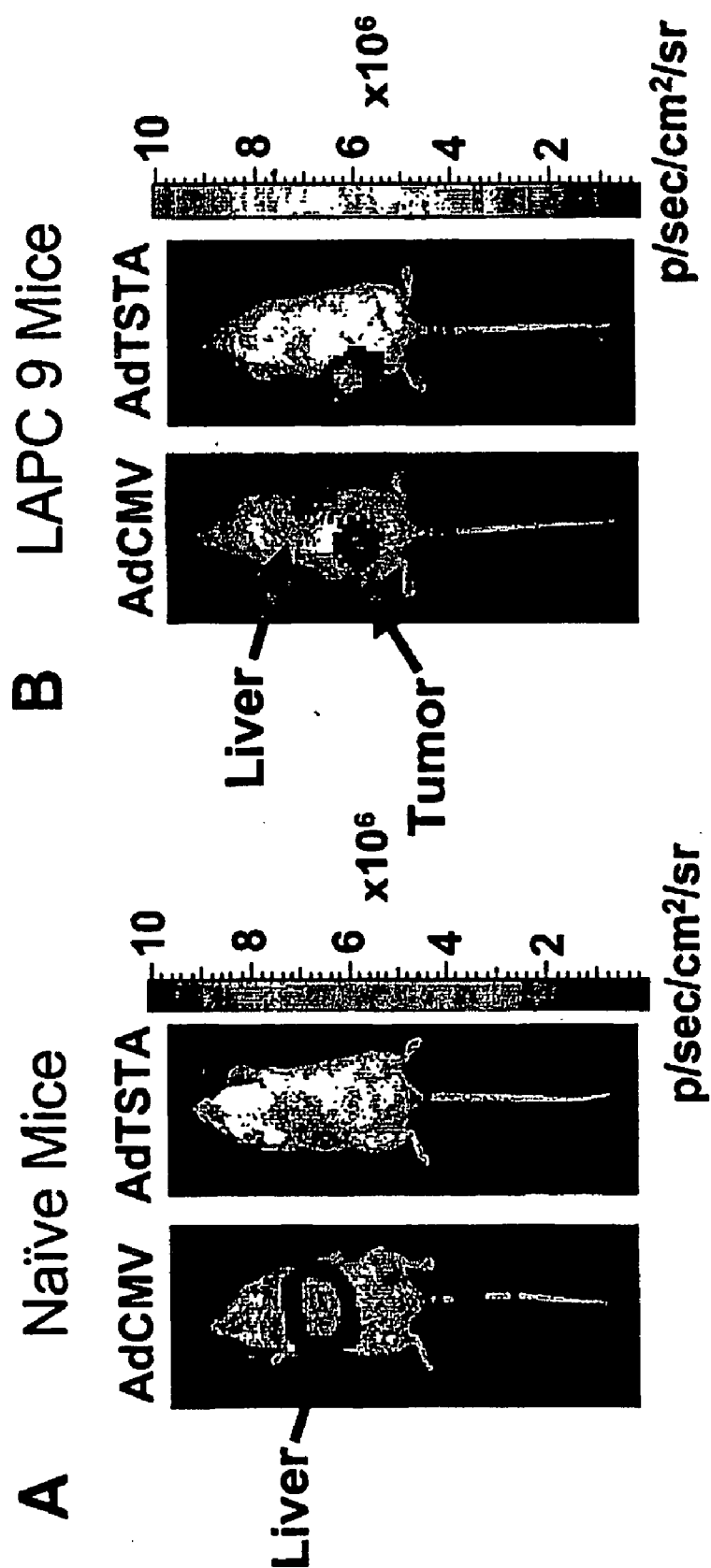


Fig. 24

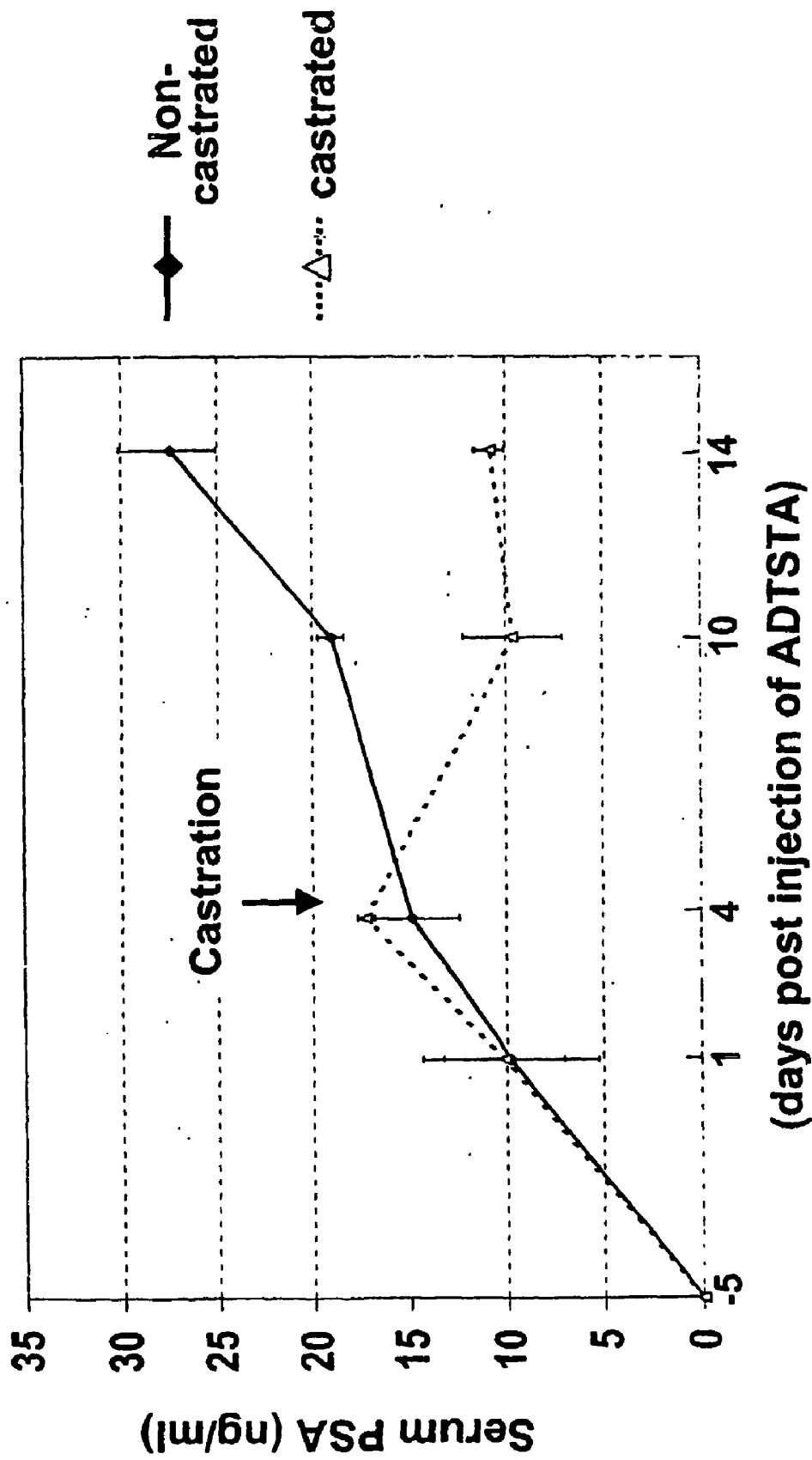


Fig. 25

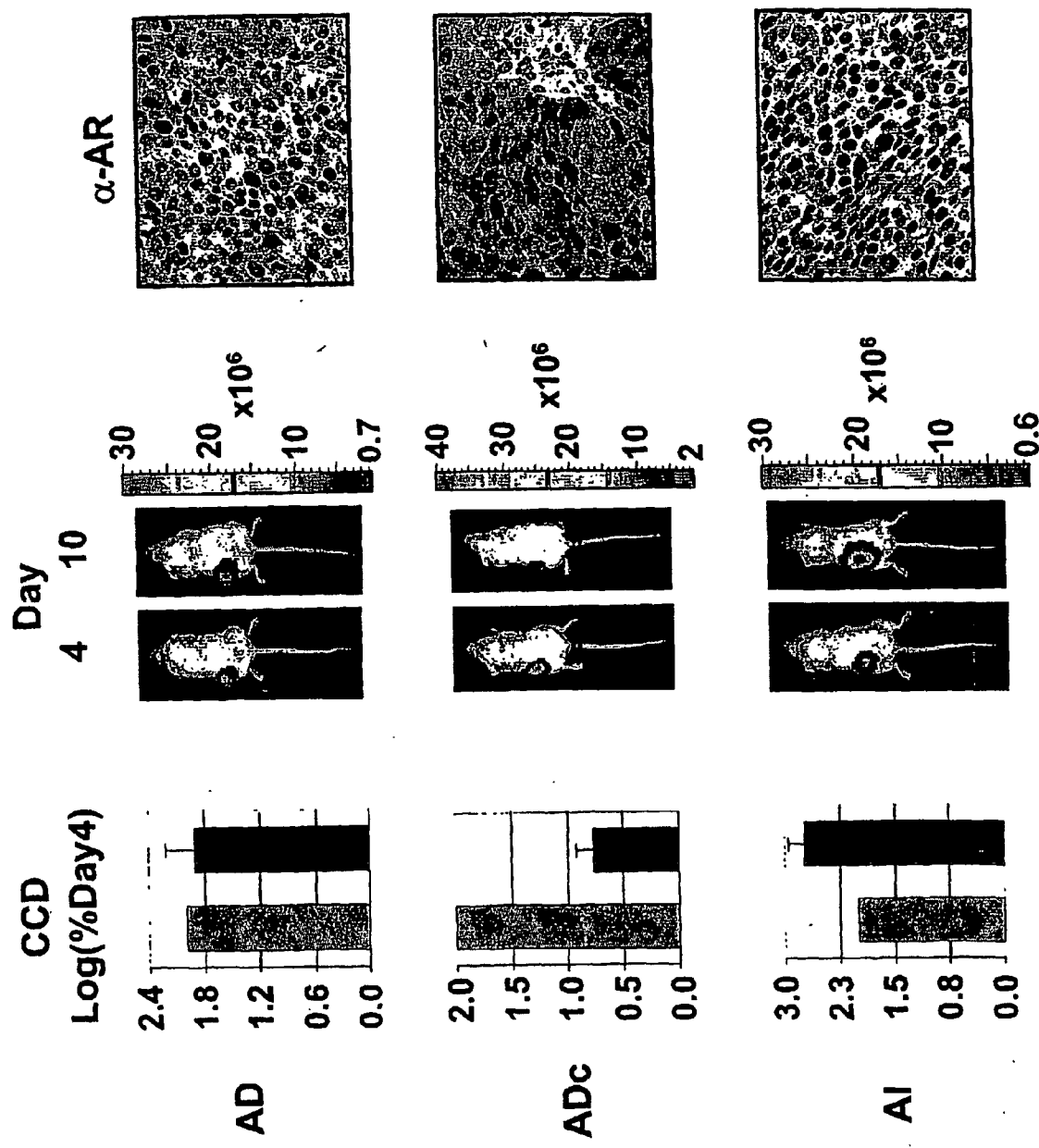


Fig. 26

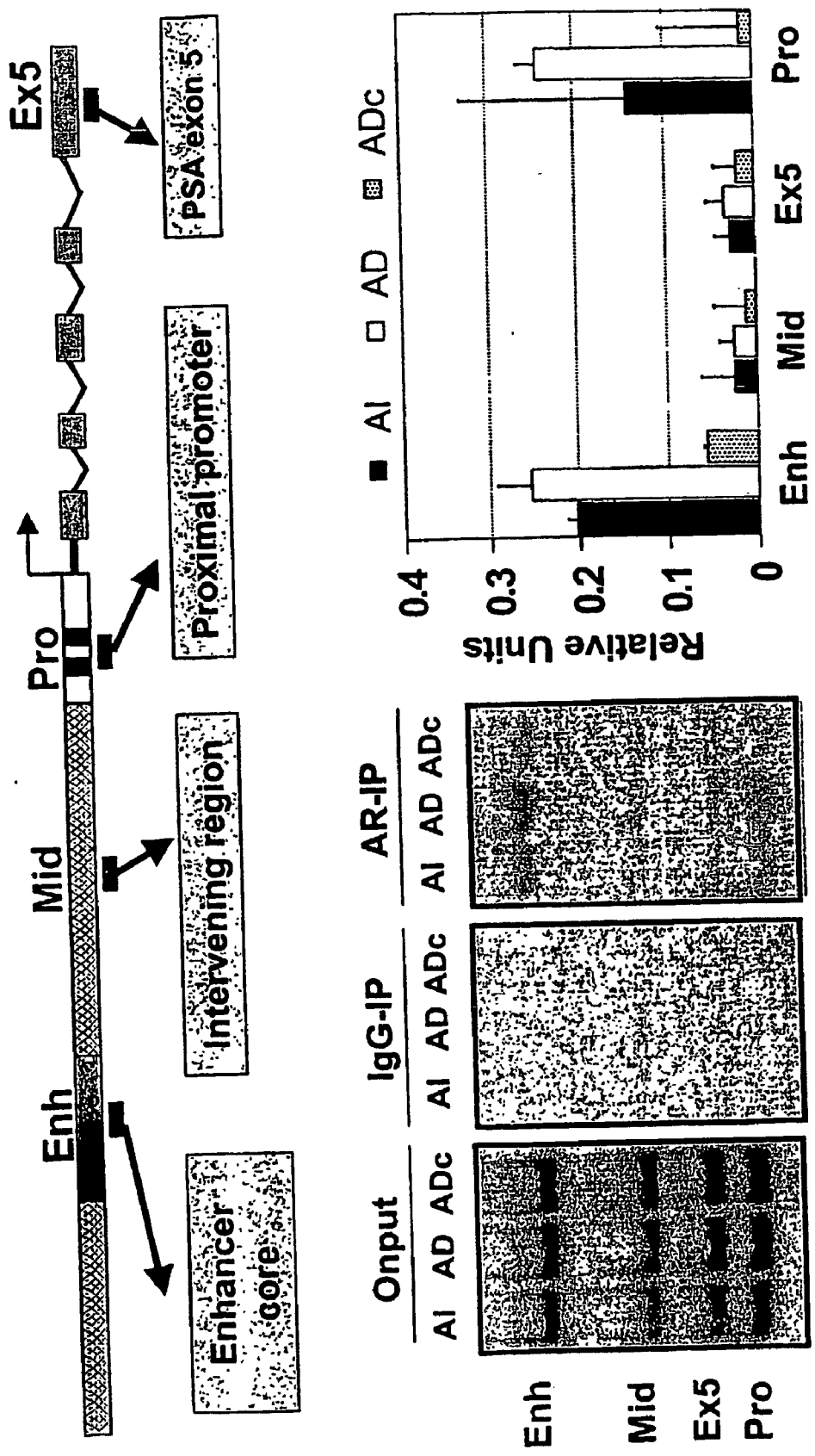


Fig. 27

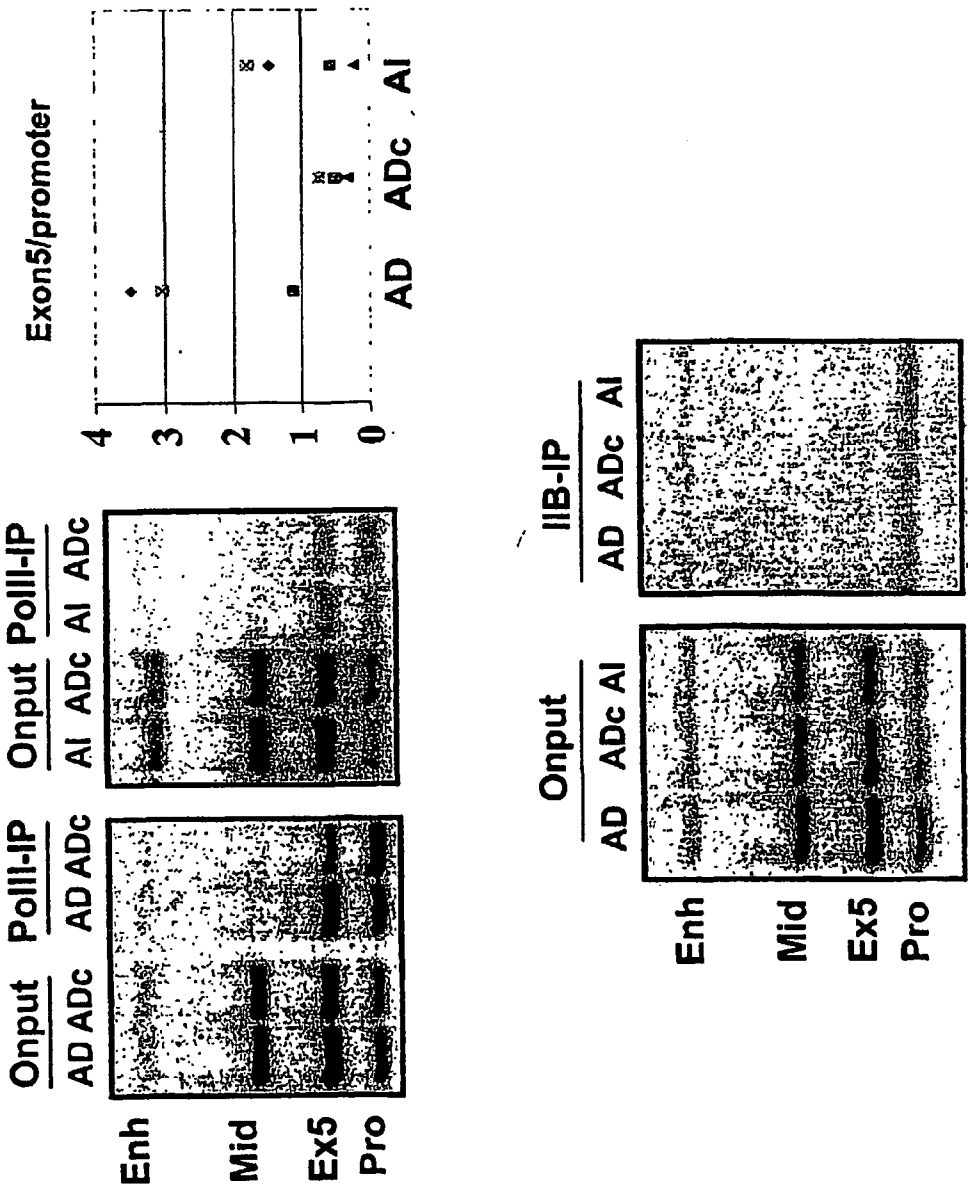


Fig. 28

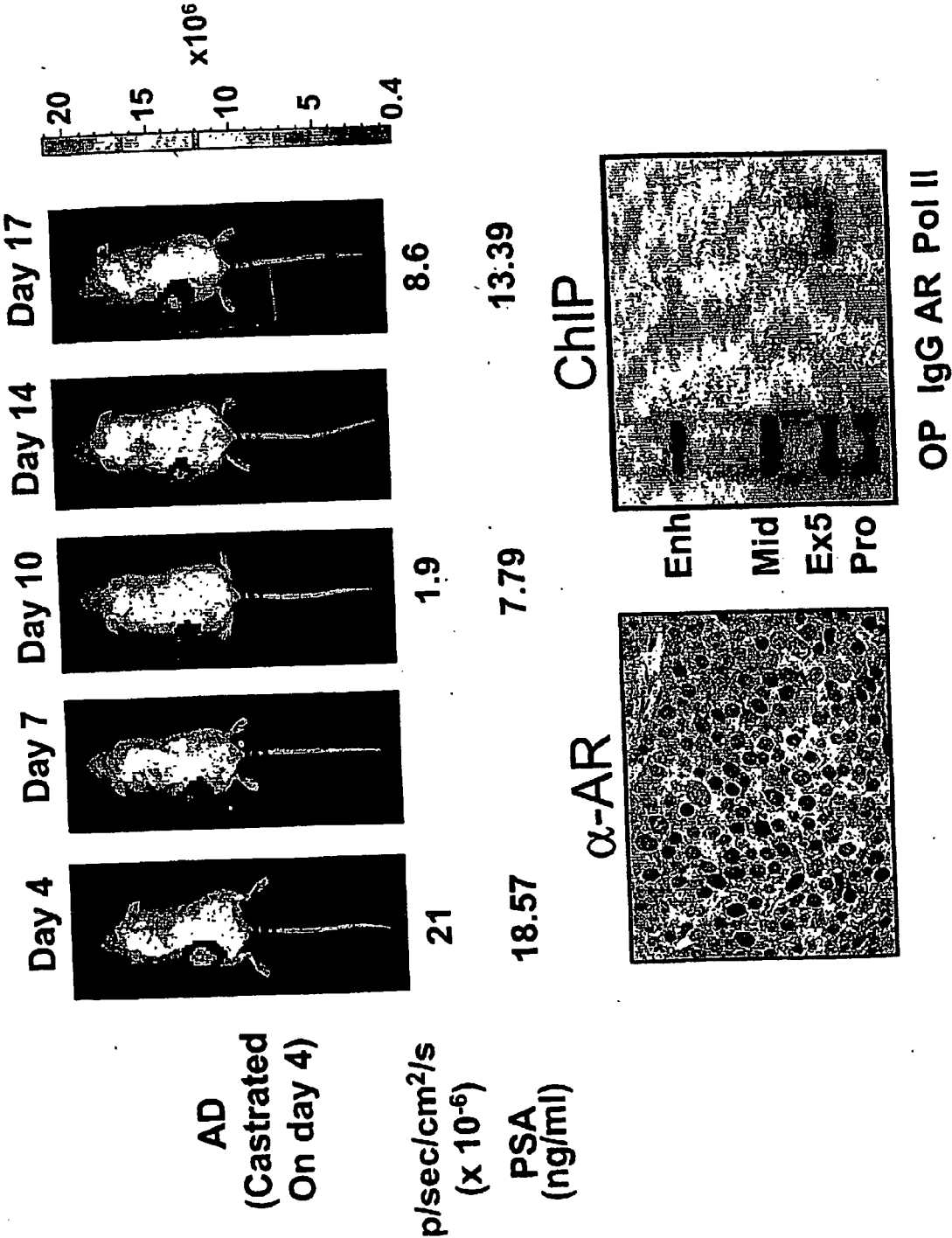


Fig. 29

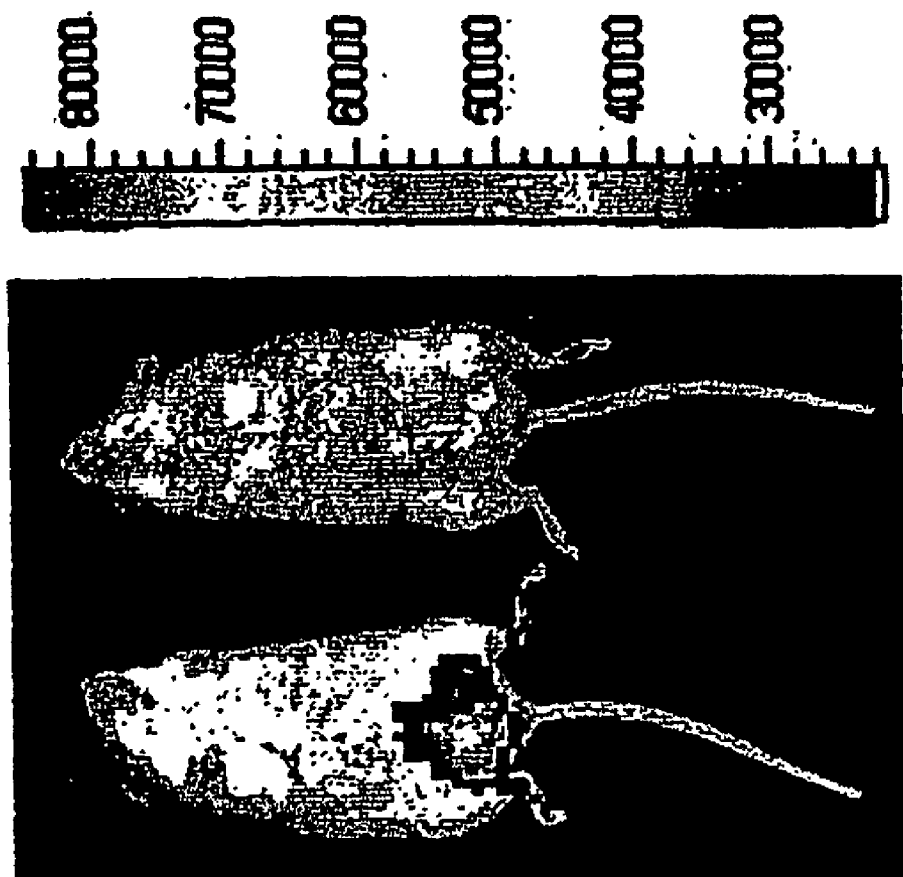


Fig. 30

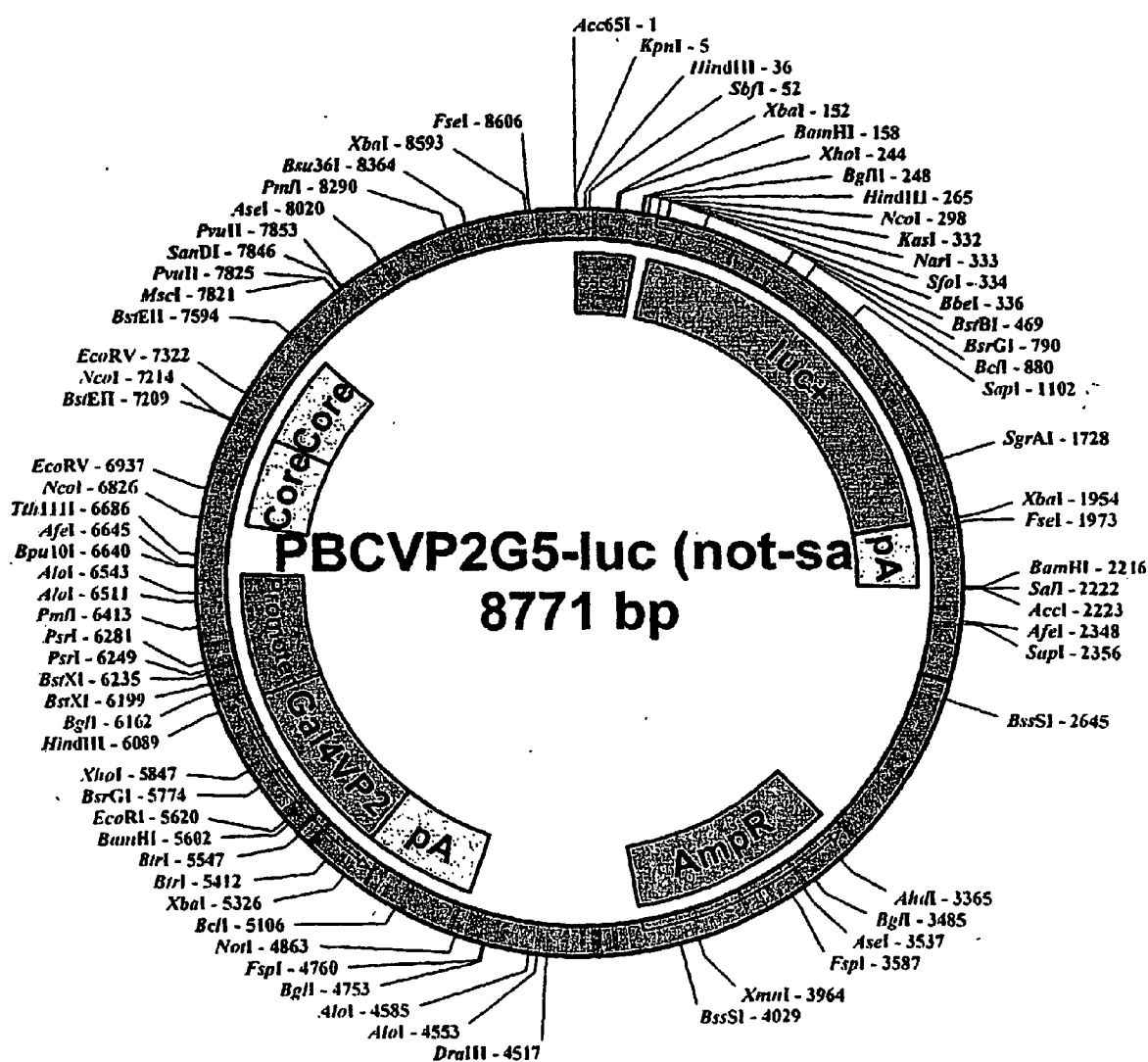


Fig. 31

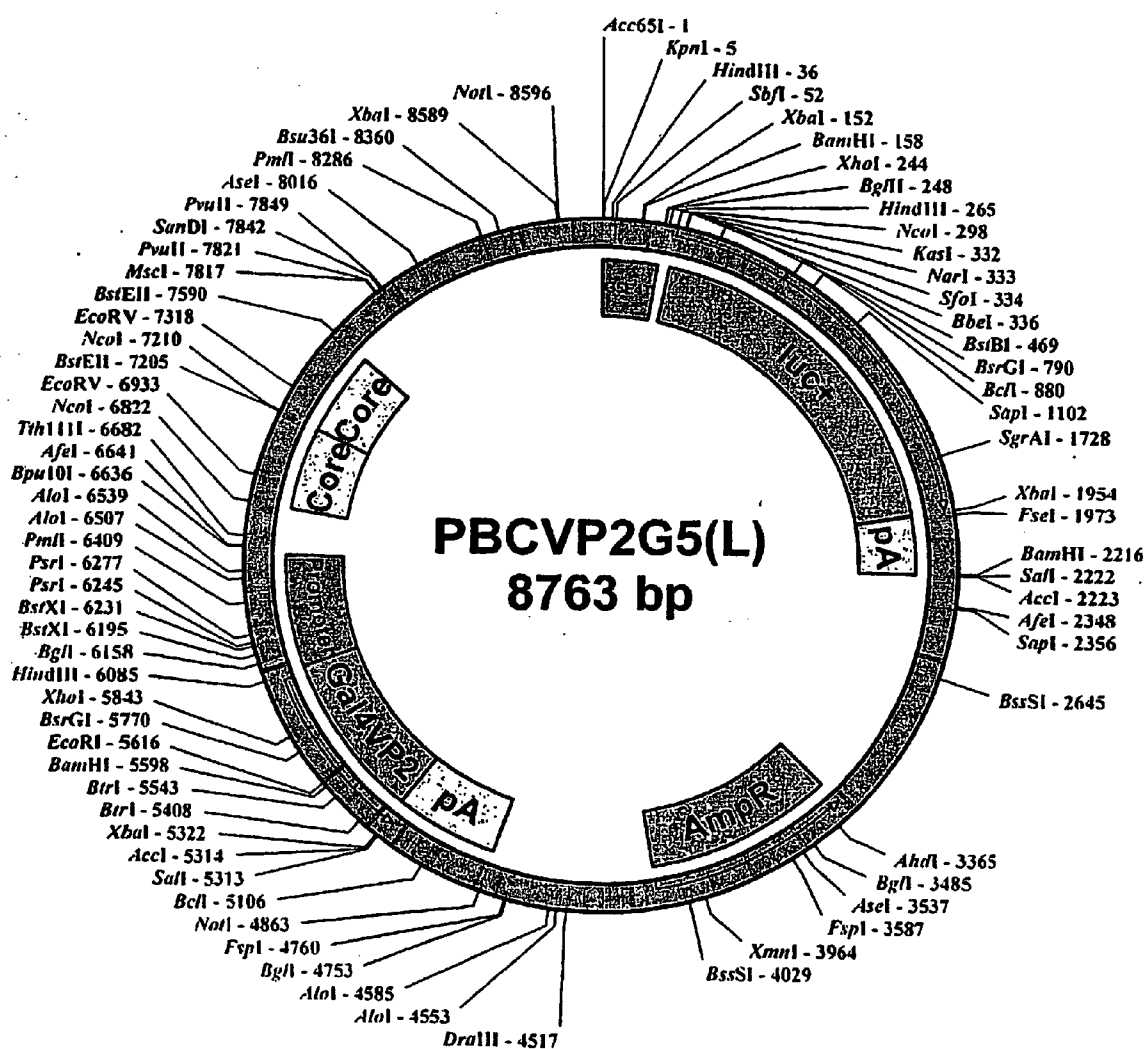


Fig. 32

TRANSCRIPTION AMPLIFICATION SYSTEM FOR MOLECULAR IMAGING

[0001] This application claims priority to provisional application, U.S. Ser. No. 60/355,300, filed Feb. 8, 2002, the contents of which are hereby incorporated by reference in their entirety into this application.

[0002] Throughout this application, various publications are referenced within parentheses. The disclosures of these publications are hereby incorporated by reference herein in their entireties.

FIELD OF THE INVENTION

[0003] The present invention relates to a transcription amplification system, comprising an effector nucleic acid molecule and a reporter molecule, which work together to produce/express a heterologous gene product in a cell-type, specific manner. The present invention also relates to methods for use of the transcription system, including methods for producing, detecting, and/or imaging the heterologous gene product.

BACKGROUND OF THE INVENTION

[0004] Current gene therapy regimens used for treatment of cancer has many limitations, including lack of tissue-specificity, borderline efficacy, and inadequate delivery methods. Most attempts to optimize gene therapy have focused on delivery of the recombinant therapeutic gene to the target tumor and restricted expression of the therapeutic gene in the target tumor. Another limitation is the lack of reliable and non-invasive methods for detecting and monitoring delivery and expression of the therapeutic gene.

[0005] One strategy for optimizing gene therapy methods includes the two-component reporter gene system, or the so-called two-step transcription amplification system (Segawa, et al., 1998 Cancer Res. 58:2282-2287). In this system, the first step involves a tissue-specific or tumor-specific promoter to drive expression of a transcription activator. In the second step, the transcription activator induces expression of a reporter or therapeutic gene product.

SUMMARY OF THE INVENTION

[0006] The present invention provides isolated, recombinant nucleic acid molecules comprising effector sequences and reporter sequences. The effector and reporter molecules comprise a two-step transcription amplification system (TSTA) which can be used to express heterologous gene products in a cell-type specific manner. The effector and reporter nucleotide sequences can be used for in vivo and in vitro production of heterologous gene products. The present invention also provides methods for making and using the nucleic acid molecules having the effector and reporter nucleotide sequences.

[0007] The effector nucleotide sequences include an upstream regulatory region which permits expression of the effector gene product in a cell-type specific manner. The upstream regulatory region is operably linked to a nucleotide sequence encoding a chimeric, transactivator protein which includes a DNA-binding domain and a transcription transactivator domain.

[0008] The reporter nucleotide sequences include a DNA-binding sequence and an upstream regulatory sequence. The

upstream sequence can be a promoter which is operably linked to a heterologous gene sequence. The heterologous gene sequence can encode a reporter gene product, a therapeutic gene product, and/or an immunologically active protein.

[0009] The chimeric transactivator protein, produced by the effector molecule, is capable of binding to the DNA-binding sequence (part of the reporter molecule) and activating transcription of the heterologous sequence. Thus, the effector gene product (e.g., the transactivator protein) is capable of trans-activating transcription, and subsequently translation (e.g., expression), of the heterologous gene sequence.

[0010] The present invention also provides methods for producing/expressing heterologous gene products using the molecules of the TSTA system. The first step includes expression of the effector gene product (e.g., the chimeric transactivator protein) in a cell-specific manner. The second step includes expression of the heterologous gene product. The effector gene product causes expression of the heterologous gene product. The heterologous gene product is produced in a cell, in a cell in a subject, or in a donor cell implanted in a subject.

[0011] The present invention provides methods for detecting production of the heterologous gene product. Such detecting methods include using non-invasive techniques, including positron emission tomography (PET), single photon emission computed tomography, cooled charged coupled device (CCD) camera optical imaging, magnetic resonance imaging, bioluminescent optical imaging, and fluorescence optical imaging.

[0012] The effector and reporter nucleotide sequences of the present invention are DNA or RNA. Further, the invention includes nucleotide sequences that are identical or nearly identical (e.g., similar) with the effector and reporter nucleotide sequences of the invention. The invention additionally provides polynucleotide sequences that hybridize under stringent conditions to the effector and reporter nucleotide sequences of the invention. A further embodiment provides polynucleotide sequences which are complementary to the effector and reporter nucleotide sequences of the invention. Yet another embodiment provides effector and reporter nucleotide nucleic acid molecules that are labeled with a detectable marker. Another embodiment provides recombinant nucleic acid molecules, such as a vector or a fusion molecule, including the effector and reporter nucleotide sequences of the invention.

[0013] The present invention provides various effector and reporter nucleotide sequences, fragments thereof having essential gene activity, and related molecules such as anti-sense molecules, oligonucleotides, peptide nucleic acids (PNA), fragments, and portions thereof.

[0014] The present invention relates to the inclusion of the effector and reporter nucleotide sequences included in an expression vector. The expression vector can be used to transform host cells or organisms to produce transgenic hosts. The invention further provides host-vector systems and transgenic animals harboring the effector and reporter nucleotide sequences. Such transgenic hosts are useful for the production, detection, monitoring, imaging, and visualizing the expression of the heterologous gene product.

BRIEF DESCRIPTION OF THE FIGURES

[0015] FIG. 1: Shows schematic diagram of the TSTA system. The first step involves the tissue-specific (e.g., PSE) expression of the GAL4-VP16 fusion protein. In the second step, GAL4-VP16, in turn, drives target gene expression under the control of GAL4 response elements in a minimal promoter [shown are five GAL4 binding sites (bs)]. Transcription of the reporter gene, either fl or HSV1-sr39tk, leads to reporter protein, which in turn leads to a detectable signal in the presence of the appropriate reporter probe. The use of the GAL4-VP16 fusion protein can potentially lead to amplified levels of the reporter protein (FL or HSV1-sr39TK) and therefore an increase in imaging signal.

[0016] FIG. 2: (A) TSTA system-mediated amplification of fl expression. LNCaP cells were transiently transfected in the absence (–L) and presence (+L) of androgen with (i) reporter construct alone (L5), (ii) PL (one-step), (iii) PG/L5 (two-step), and (iv) SG/L5 (control) constructs. The cells were harvested 48 h after transfection and assayed for FL activity. The error bars represent SEM for triplicate measurements. (B) Cell-type specificity of the TSTA system (fl). C6, HeLa, and LNCaP cells were transiently transfected in the absence (–L) and presence (+L) of androgen with effector construct, PG, and reporter construct, L5. The cells were harvested 48 h after transfection and assayed for FL activity. The error bars represent SEM for triplicate measurements.

[0017] FIG. 3: (A) TSTA system-mediated amplification of HSV1-sr39tk expression. LNCaP cells were transiently transfected in the absence (–L) and presence (+L) of androgen with (i) reporter construct alone (T5), (ii) PT (one-step), (iii) PG/T5 (two-step), and (iv) SG/T5 (control) constructs. The cells were harvested 48 h after transfection and assayed for HSV1-sr39TK activity. The error bars represent SEM for triplicate measurements. (B) Cell-type specificity of the TSTA system (HSV1-sr39tk). C6, HeLa, and LNCaP cells were transiently transfected in the absence (–L) and presence (+L) of androgen with the effector construct, PG, and reporter construct, T5. The cells were harvested 48 h after transfection and assayed for HSV1-sr39TK activity. The error bars represent SEM for triplicate measurements. (C) Effect of androgen concentration on HSV1-sr39tk expression. LNCaP cells were transiently transfected in the absence (–L) and presence (+L) of androgen with PG and T5. The androgen concentration varied from 0.1 to 10 nM. The cells were harvested 48 h after transfection and assayed for HSV1-sr39TK activity. The error bars represent SEM for triplicate measurements.

[0018] FIG. 4: (A) In vivo optical CCD imaging of mice carrying transiently transfected LNCaP cells for control studies. All images shown are the visible light image superimposed on the optical CCD image with a scale in RLU/min as shown. (Panel 1) LNCaP cells were transiently transfected with only the L5 vector (control) and cells implanted i.p. The animal was then imaged after injection of D-luciferin (i.p.). (Panel 2) The same animal as in Panel 1 was imaged 48 h after implantation of androgen pellet by re-administering D-luciferin (i.p.). (Panel 3) LNCaP cells were transiently transfected with the PG and L5 vectors and cells implanted i.p. The mouse was imaged after i.p. injection of D-luciferin. (Panel 4) The same animal imaged in Panel 3 was re-imaged in the absence of androgen 48 h later after i.p.

injection of D-luciferin. (B) In vivo optical CCD imaging of mice carrying transiently transfected LNCaP cells for comparison of one-step and TSTA. All images shown are the visible light image superimposed on the optical CCD image with a scale in RLU/min as shown. (Panel 1) LNCaP cells were transiently transfected with only the one-step PL vector and cells implanted i.p. The animal was then imaged after injection of D-luciferin (i.p.). (Panel 2) The same mouse in Panel 1 was re-imaged with i.p. injection of D-luciferin 48 h after implantation of an androgen pellet. (Panel 3) LNCaP cells were transiently transfected with the PG and L5 vectors (TSTA system) and cells implanted i.p. The mouse was then imaged after i.p. injection of D-luciferin. (Panel 4) The same animal imaged in Panel 3 was re-imaged with i.p. D-luciferin 48 h after implantation of an androgen pellet.

[0019] FIG. 5: Shows comparison of transcriptional activation in vivo using the TSTA system versus the one-step system. Shown are results of mean±SEM RLU/min in five nude mice in each group. The first group had LNCaP cells transiently transfected with PL (one-step), and the second group had LNCaP cells transiently transfected with PG and L5 vectors (two-step). The cells were implanted i.p. in the mice. The mice were then implanted with androgen pellets and imaged again after 24 and 48 h. There is a significant difference (* P<0.05) between the two groups.

[0020] FIG. 6: Components of the Chimeric TSTA System. This figure illustrates the theory and design of the TSTA system. (A) Depiction of the two-step transcriptional activation process. In the first step, GAL4-VP16 derivatives (oval circles) are expressed in prostate cancer cells in the presence of androgen (R1881), which activates the PSA enhancer, PSE. In the second step, GAL4-VP16 binds to a GAL4-responsive promoter, and activates expression of luciferase. (B) This panel illustrates the effector plasmids used in our analysis. We describe the detailed composition in Results and in Materials and Methods. The abbreviations denote the components: GAL4: GAL4 DNA Binding Domain. VP16 AD: VP16 activation domain. Enhancer refers to the 390-bp core region bearing multiple AREs [10]; AREI and II are proximal AREs found in the promoter described by Trapman and colleagues [44]; the GAL4-VP1 to -VP4 derivatives are as described [68]. E4TATA contains the adenovirus E4 minimal promoter from –38 to +38 relative to the start site. (C) The FL reporters used in the analysis (described in Results). (D) The single construct comprises the G5-L plasmid with the PBC-VP2 fragment inserted into the NotI site.

[0021] FIG. 7: Comparison of Two-step vs. One-step. We grew LNCaP cells in 6-well tissue culture plates and transiently transfected them with G5-L reporter and PSE/PBC-driven GAL4-VP1 (two-step), or with luciferase reporter driven directly by PSE/PBC (one-step). We added 10 nM R1881 (synthetic androgen) to the “+ligand” samples one hour after transfection, and measured the luciferase activities 48 hours after stimulation. The experiments were repeated multiple times in triplicate. The measurements shown here are average values of a representative experiment. The vertical axis shows the relative light unit (RLU) reading from the luminometer. The error bars represent standard deviation.

[0022] FIG. 8: Increasing the Number of GAL4 Sites and VP16 Domains Augments Activity. We transfected LNCaP

cells with PSE-VP1 (left panel) or PBC-VP4 (right panel) and G1-, G2- and G5-L. We treated and measured the cells as in **FIG. 7**. The measurements shown in the two panels are from a side-by-side experiment.

[0023] FIG. 9: Comparing Different Numbers of Activation Domains. We transfected LNCaP cells with G5-L and either GAL4-VP1, -VP2 or -VP4 expression vectors driven by the PSE or chimeric (PBC) PSA enhancer-promoter. SV40-VP4/G5-L and CMV-L serve as benchmarks. We adjusted the DNA concentrations so that the transfections contained comparable molar amounts of the FL gene.

[0024] FIG. 10: The Spectrum of Activities Generated by the TSTA System. We plotted results of the previous experimental combinations side-by-side for direct comparison. We normalized the measurements to CMV-L activity in the presence of R1881. CMV-L was assigned a value of 1. The samples are aligned by their activities. 1. PSE-L 2. PSE-VP1/G1-L 3. PBC-VP4/G1-L 4. PBC-L 5. PSE-VP1/G2-L 6. PBC-VP4/G2-L 7. PSE-VP1/G5-L 8. PBC-VP1/G5-L 9. PBC-VP4/G5-L 10. PBC-VP2/G5-L 11. CMV-L 12. SV40-VP4/G5-L.

[0025] FIG. 11: Cell Specific Expression and Androgen Inducibility of the TSTA system. (A) Immunoblot analyses demonstrating the expression GAL4-VP2 from the optimized PBC-VP2 construct versus our benchmark SV40-VP2. We transfected LNCaP cells with PBC-VP2/G5-L or SV40-VP2/G5-L with or without androgen treatment. The samples were prepared, blotted and probed with GAL4-VP16 antibodies. (B) We seeded six human cell lines in six-well plates and transfected as described. The same molar amount of luciferase gene was transfected into all the cell types with a total DNA amount of 0.5 mg per well. We normalized all the RLU readings to the values obtained from the combination of SV40-VP2 and G5-L transfected into the same cell line. The SV40-VP2/G5-L value was set at 1 in the 3-D plot. We employed PBC-L as a control for promoter specificity of the effector and measured the background by transfection of G5-L alone.

[0026] FIG. 12: Cell Specific Expression of the Single Construct. We transfected six human cell lines with SV40-VP2/G5-L, PBC-VP2/G5-L or the single construct. All the cells were transfected with the same molar amount of luciferase DNA. The cells were sampled, analyzed and graphed as in **FIG. 11** except we switched the axes on the cell lines and transfected plasmids to simplify the presentation.

[0027] FIG. 13: Imaging of One-step and TSTA in Living Athymic Nude Mice. Pictures shown in the figure are bioluminescent color images superimposed upon the gray-scale mouse photographs. The color scale is in units of RLU/min and is to the right of each photo. Note that the scales vary among experiments. A map representing the dorsal surface of the mice is on the left; the circles denote the relative position of the three injection spots, with the transfected plasmids labeled over each circle. We also marked the needle points on the mouse with a red marker. A description of the group is shown on top of each panel and the acquisition time of the CCD camera for each image generated is in parentheses.

[0028] FIG. 14: Luciferase expression patterns in mice and adenoviral vector-mediated luciferase gene delivery to

the liver after systemic administration. (A) CCD images of mice injected with either AdCMV-luc or the prostate-specific AdPSE-BC-luc via tail vein. The images for 2 representative animals from each cohort at 4 days post-injection are shown. The animal designation in each cohort is indicated above the images. BC1 and BC3 represent mouse #1 and #3, respectively, in the cohort that received AdPSC-BC-luc, and CMV4 and CMV5 indicate the AdCMV-luc injected animals. The relative light intensity (RLU/min) emitted from the animal was quantitated by computer image analysis software and represented by the color scale ranges from violet (least intense) to red (most intense), shown next to the images. The maximal signal intensity (maximum RLU/min) for each image is shown below each image. Liver signals in the AdCMV-luc cohort were more than 5 orders of magnitude higher than the AdPSE-BC-luc group. (B) Adenoviral gene transferred in livers of cohorts injected either with AdCMV-luc or AdPSE-BC-luc. Southern blot analysis of total cellular DNA, extracted from the livers of same animals in the 2 treatment cohorts, as in **FIG. 14A**, after imaging at 4 days post-injection. DNA (2 and 10 μ g) of each sample was analyzed.

[0029] FIG. 15: Kinetics of transgene expression and detection of metastatic lesions in living mice bearing androgen-dependent (AD) LAPC-4 tumors. (A) Location and magnitude of luciferase expression over 3 weeks' duration after intra-tumoral injection of AdCMV-luc. The format of image display is similar to that described in **FIG. 14A**. However, all images are results of a single mouse, CMV1, monitored on sequential days after Ad injection (indicated at the top of each image). Two clear sites of luciferase expression detection are in the liver (indicated by (l) after signal intensity) and in the tumor (t). Tumor signals at 15 and 21 days post-injection were below the minimal scale ($1E+5$) set. Thus, using these imaging parameters the signals in the tumor was unable to be determined (UTD). (B) The in vivo luciferase expression profile of an AdPSE-BC-luc-injected animal (BC4). The in vivo luciferase expression was monitored at specific days post intra-tumoral injection (listed above the image). The signal intensity of the tumor (t) and of extra-tumoral lesions (e) is listed below the respective images. The signal in the animal at 2 days post-infection, before the onset of expression, served as background luminescence signal (≤ 70). Extra-tumoral signals were detected at 21 days post-injection. (C) The CCD images of freshly isolated organs from mouse BC4. Individual organs of BC-4 (same as **FIG. 15B**) were isolated and re-imaged. Due to light signal attenuation contributed by the covering tissues, the isolated organs displayed higher signal intensities than in the intact living animal¹².

[0030] FIG. 16: Detailed histological analysis of spinal and lung metastatic lesions. (A) Histological analysis of the spine lesion of mouse BC4. 5- μ m sections of spine were stained with hematoxylin/eosin (H&E) or with human-specific anti-cytokeratin antibody. Unmagnified sections show an elongated lesion in the mid-segment of the spine. A low-magnification (40 $\times$) micrograph showed the lesion was surrounded by muscle (Mu) and adjacent to bone (Bo). Higher magnifications (200 $\times$ and 400 $\times$) of the lesion were displayed. Anti-human cytokeratin specifically stained the lesion with a characteristic intense ring of cytoplasmic staining. (B) Corresponding CCD signal and histological analysis of a spinal lesion in another mouse BC2. Procedures for the detection and identification of the lesion are as

described above. (C) Detection of lung metastasis by CCD imaging in another animal, and definition of the lesion by confocal microscopy. Low-intensity upper chest signals, right>left, were detected in a LAPC4 AI tumor-bearing mouse (BC1) 21 days after intra-tumoral injection of AdPSE-BC-luc under the same conditions as in FIG. 15.

[0031] FIG. 17: Expression of endogenous and exogenous androgen receptor (AR)-regulated genes in an androgen-independent (AI) prostate tumor. (A) Endogenous AR and PSA expression in AD and AI LAPC-4 tumors. The brown staining indicates positive protein expression. PSA expression in AI tumor appears to be elevated compared to the AD LAPC-4 tumor. (B) CCD images of LAPC-4 AD or AI tumor-bearing mice 11 days after intra-tumoral injection. The images of 3 representative animals from each cohort are shown. The AI tumors are derived from two independent tumor passages. BC3A is a different passage from BC2 and BC3. (C) AdPSE-BC-luc-mediated luciferase expression in LAPC-4 AD and AI tumor cell suspensions after ex vivo infection. The graph displays the luciferase activity of infected cell extracts harvested at 3 days post-infection. Statistical analysis by t-test showed a significant difference ($P=0.007$) (two-tail). Single-cell suspension cultures were infected at 10 infectious units/cell and analyzed at three days post-infection⁸.

[0032] FIG. 18: Shows A schematic diagram is represented for two approaches for imaging of reporter gene expression using PET/SPECT. A reporter gene introduced into the cell can encode for (I) an enzyme (e.g., HSV1-TK) that leads to trapping of a radiolabeled probe (left panel) or (II) an intracellular and/or extra cellular receptor (e.g., D₂R), which would lead to trapping of a radiolabeled ligand (right panel). In both cases if the reporter gene is not expressed, then the radiolabeled probe is not retained.

[0033] FIG. 19: Shows MicroPET imaging of two PET reporter genes (HSV1-tk and D₂R) in the same mouse using two different reporter probes (¹⁸F labeled FPCV and FESP) respectively. Specific accumulation of probes in a mouse carrying a tumor stably expressing HSV1-tk (right) and a separate tumor stably expressing D₂R (left). The accumulation of [¹⁸F]FPCV and [¹⁸F]FESP in each tumor reflects trapping due to HSV1-tk and D₂R expression respectively. Background signal in the intestinal tract is seen due to clearance of the probes via the hepatobiliary system. A separate scale for [¹⁸F]FPCV and [¹⁸F]FESP is shown (135).

[0034] FIG. 20: Shows A schematic representation of imaging reporter gene expression by PET from a bi-cistronic vector containing an internal ribosomal entry site (IRES) (left panel). Both gene A and B are co-expressed from the same vector with the help of the IRES and expression of protein B (a PET reporter) can be imaged quantitatively by trapping of a PET reporter probe which will give an indirect measurement of expression of gene A. MicroPET imaging of bi-cistronic gene expression (pCMV-D₂R-IRES-sr39tk) where both the genes were imaged by using two different PET reporter probes ([¹⁸F]FESP and [¹⁸F]FPCV) in same animal (right panel). Three C6 cell lines stably transfected with pCMV-D₂R-IRES-sr39tk and the parental C6 control cell line were injected at 4 different sites in a single mouse. Sequential imaging of the tumors with [¹⁸F]FDG, [¹⁸F]FESP and [¹⁸F]FPCV after 10 days showed specific accumulation of [¹⁸F]FESP and [¹⁸F]FPCV in the tumors with stably

transfected cells while accumulation of [¹⁸F]FDG is seen in all four tumors in the FDG section image. The [¹⁸F]FDG (whole body) image shows the mouse outline and is provided for reference. The [¹⁸F]FESP and [¹⁸F]FPCV tumor images are highly correlated, illustrating that when one monitors one of the two genes, one can infer levels of the second gene (144).

[0035] FIG. 21: (A) Shows the nucleotide and amino acid sequence of a vector comprising the effector and reporter sequences (PBCVP2G5 (not Sal)). (B) Shows the nucleotide and amino acid sequence of a vector comprising the effector and reporter sequences (PBCVP2G5-L).

[0036] FIG. 22: The adenovirus two-step transcription activation (AdTSTA) imaging system. The upper portion of the diagram shows the TSTA imaging cassette. The PSA enhancer from -4326 to -3935 (purple) was duplicated (the chimeric enhancer core) within the upstream regulatory region from -5322 to -3744 and attached to the proximal promoter from -541 to 1. Each enhancer bears a cluster of six AREs and the promoter contains two AREs shown in blue. The PSA regulatory region is shown expressing GAL4-VP2 bearing two amino-terminal Herpes Simplex Virus 1 VP16 activation domains (amino acids 413-454) fused to the GAL4 DNA binding domain (amino acids 1-147). A GAL4-responsive promoter is fused in the divergent orientation to the PSA regulatory region. The GAL4-responsive promoter contains five 17-bp GAL4 sites upstream of the adenovirus E4 promoter driving firefly luciferase. The entire cassette was cloned into a shuttle vector and introduced into Ad5 deleted (.) for E1 and E3 using the AdEasy™ system. The virus was propagated in 293 cells, purified and titered. ITR Inverted terminal repeat. Bottom: simplified representation of Adenovirus serotype 5.

[0037] FIG. 23: AdTSTA activity in cancer cell lines. A. LNCaP cells were infected with AdTSTA at an MOI of 10 for 1 hour and treated with 10 nM R1881 (+Ligand) or vehicle (-Ligand). At the indicated time points, the cells were lysed with Reporter Lysis Buffer and firefly luciferase activity was analyzed either by luminometry (lower panel, Y-axis: Relative Luciferase Units/μg of total protein normalized to 100%) or by immunoblotting (Upper panel, AR: Anti-Androgen Receptor; Tub: Anti-Tubulin; GAL4: anti-GAL4-VP16). Samples were prepared in triplicate and the average reading with standard error is shown. The triplicate samples were mixed for immunoblot analysis. B. LNCaP, HeLa or HepG cells were infected with AdTSTA at an MOI of 0.1 for 1 hour followed by treatment with 10 nM R1881. The cells were harvested 48 hours later and luciferase levels were measured. Data are normalized to the ligand-induced signal in LNCaP (100%). The AdCMV (MOI 0.1) signal in LNCaP is shown in hatched bars for comparison of the AdTSTA and AdCMV luciferase activity.

[0038] FIG. 24: AdTSTA specificity in animals. Left panel: 107 pfu of AdCMV or AdTSTA virus were injected through the tail vein into 3-month old male SCID mice and imaged by CCD. The pictures show a representative mouse in the supine position injected with AdCMV or AdTSTA on day 14. Right panel: LAPC9 AD xenografts were grown on the flanks of SCID mice. When tumors reached 0.5 cm diameter tumor size, AdCMV or AdTSTA were injected intratumorally and imaged by CCD. The picture shows representative mice in the prone position on day 14. For all

studies, $n > 3$ animals were used in each group. For each mouse, a pseudocolor image of the emitted light is superimposed over a gray scale photograph of the mouse. A colored bar, which indicates the intensity of the signals, is shown on the right of the panels, with units of photons (p) acquired per second (sec) per cm^2 per steradian (sr).

[0039] FIG. 25: Serum PSA Measurements for AD and Castrated Mice. Serum Elisa measurements of PSA at various time points during tumor growth. Values are in ng per ml.

[0040] FIG. 26: AR signaling in LAPC 9 tumors. SCID mice implanted with LAPC9 xenografts grown to greater than 0.5 cm were injected with 107 pfu of AdTSTA and the mice were imaged every 3-4 days until day 14. Representative mice at day 4 and day 10 post virus injection from the AD group, the castrated (on day 4) AD group (ADc), and the stable AI group. The bar graph summarizes a cohort of three or more and summarizes the log of the % change in signal from day 4 (blue bars) to day 10 (purple bars). Day 4 is set at 2 (log of 100) in each case. The right panels show representative immunohistochemical localization of AR in the various tumors using anti-AR antibodies. AR stains brown against the blue-stained nuclei.

[0041] FIG. 27: Chromatin immunoprecipitation assays in LAPC9 tumors. The diagram describes the PSA regulatory region. Short black line underneath indicates the positions targeted by PCR. Enh: enhancer core; Mid: intermediate region; Pro: proximal promoter; Ex5: PSA exon 5 (for sequence coordinates see Methods). Tumors were isolated from mice sacrificed at day 10 (6 days post castration for ADc), minced, crosslinked with formaldehyde and immunoprecipitated with anti-AR. An autoradiograph of the multiplex PCR reactions is shown for AD, AI and ADc tumors. Graph of Multiple Tumor ChIP Analyses. The band intensities were analyzed using ImageQuant. Background values from a mock (IgG) ChIP were subtracted from each band and normalized to the signal from onput DNA. Error bars shown are standard deviation of three values obtained in independent experiments.

[0042] FIG. 28: ChIP analysis of RNA Polymerase II and TFIIB from LAPC9 tumors. The bands are described in the **FIG. 27** legend. Representative experiments from AD, AI and ADc tumors are shown. The top panels are pol II and the bottom panels are TFIIB. The scatter plot represent the pol II binding from 4 experiments, where the ratios of pol II binding at exon 5 vs. the proximal promoter are shown.

[0043] FIG. 29: Dynamic AR signaling. A SCID mouse bearing an LAPC9 AD tumor was injected with AdTSTA, imaged and castrated as described previously. The upper panel shows the entire time course with signals adjusted to the same color scale. Imaging measurements and PSA levels determined by Serum ELISA are shown below the images. Lower left panel: the tumors were extracted and subjected to immunohistological staining with AR antibodies. Lower right panel: a ChIP assay of the extracted tumors with IgG, AR and pol II antibodies.

[0044] FIG. 30: Shown are a male transgenic mouse (left) and control mouse (right) imaged with D-Luciferin using a cooled CCD Camera. The color scale represents the relative light units for bioluminescence signal. Note the bioluminescence from the region of the prostate in the transgenic

mouse. This illustrates the use of the TSTA approach in imaging prostate specific expression of a firefly luciferase optical reporter gene.

[0045] FIG. 31: A schematic diagram of a vector including the effector and reporter nucleotide sequences (PBCVP2G5-luc (not -sal))

[0046] FIG. 32: A schematic diagram of a vector including the effector and reporter nucleotide sequences (PBCVP2G5(L)).

DETAILED DESCRIPTION OF THE INVENTION

[0047] In order that the invention herein described may be more fully understood, the following description is set forth.

[0048] The term “isolated” as used herein means a specific nucleic acid or polypeptide, or a fragment thereof, in which contaminants (i.e. substances that differ from the specific nucleic acid or polypeptide molecule) have been separated from the specific nucleic acid or polypeptide.

[0049] As used herein, a first nucleotide or amino acid sequence is said to have sequence “identity” to a second reference nucleotide or amino acid sequence, respectively, when a comparison of the first and the reference sequences shows that they are exactly alike.

[0050] As used herein, a first nucleotide or amino acid sequence is said to be “similar” to a second reference sequence when a comparison of the two sequences shows that they have few sequence differences (i.e., the first and second sequences are nearly identical). For example, two sequences are considered to be similar to each other when the percentage of nucleotides or amino acids that differ between the two sequences may be between about 60% to 99.99%.

[0051] The term “complementary” refers to nucleic acid molecules having purine and pyrimidine nucleotides which have the capacity to associate through hydrogen bonding to form double stranded nucleic acid molecules. The following base pairs are related by complementarity: guanine and cytosine; adenine and thymine; and adenine and uracil. Complementary applies to all base pairs comprising two single-stranded nucleic acid molecules, or to all base pairs comprising a single-stranded nucleic acid molecule folded upon itself. Molecules may be fully or partially complementary to the molecules of the invention.

[0052] The term “fragment” of an effector or a reporter nucleic acid molecule refers to a portion of the effector or reporter nucleotide sequences of the invention. A fragment of an effector or reporter molecule, is therefore, a nucleotide sequence having fewer nucleotides than and/or modified from the effector or reporter nucleotide sequences of the invention.

[0053] The term “operably linked” as used herein refers to two or more nucleotide sequences which are juxtaposed so as to permit function. For example, a promoter sequence operably linked to a nucleotide sequence encoding a gene product refers to the promoter sequence juxtaposed to the nucleotide gene sequence so that the promoter is capable of controlling the transcription of the gene sequence.

Effector Sequences

[0054] The present invention provides effector nucleic acid molecules including an upstream regulatory sequence operably linked to a nucleotide sequence encoding a chimeric, transcription activator protein (e.g., transactivator protein). The upstream regulatory sequence can include one or more of promoters and/or enhancers or any combination thereof.

[0055] The enhancer or promoter sequences can include portions having functions, such as nucleotide sequences that are known to bind cellular proteins or agents. The enhancer or promoter sequence function to mediate transcription of any operably linked gene sequence. These portions can be arranged within the enhancer or promoter sequences in a wild-type arrangement, or in a modified arrangement. For example, a modified enhancer or promoter sequence can include repeat sequences of a particular portion that bind cellular proteins or agents. Alternatively, the modified enhancer or promoter sequence can include repeat sequences of two or more portions. The repeat sequences can be arranged in a head-to-head or in a head-to-tail orientation. The cell-specific, upstream regulatory sequence can be intact (e.g., wild-type) or modified to include insertions, deletions, substitutions, or mutations.

[0056] The regulatory sequence can be a cell-specific regulatory sequence isolated from various cell types including: blood, prostate, brain, lung, stomach, bladder, pancreas, colon, breast, ovary, uterus, cervix, liver, muscle, skin, or bone.

[0057] The regulatory sequence can be isolated from various tissue-specific genes, including transferrin, tyrosinase and tyrosinase-related genes (melanocytes), albumin (liver), muscle creatinine kinase (muscle), myelin basic protein (oligodendrocytes and glial cells), glial fibrillary acidic protein (glial cells), and NSE (neurons).

[0058] The tumor-specific, regulatory sequence can be isolated from various tumor-specific genes, including VEGF, KDR, E-selectin, endoglin, AFP (liver tumor), CEA (various adenocarcinomas), erbB2 (breast and pancreatic cancer), muc-1(DF3) (breast cancer), ALA (breast cancer), BLG (breast cancer), osteocalcin (osteosarcoma and prostate cancer), SLP1 (ovarian and cervical cancer), HRE (solid tumors), Grp78(BIP) (solid tumors), L-plastin (cancer cells), and hexokinase II (cancer cells).

[0059] The regulatory sequences can be isolated from treatment responsive genes (egr-1, t-PA, mdr-1, hsp70) or from cell cycle-regulated genes (E2F-1, cyclin A, and cdc25C). See Nettelbeck for a review (Trends in Genetics (2000) 16:174-181).

[0060] The regulatory sequences can be from any viral source, including adenovirus, adenovirus-associated virus, retrovirus, and lentivirus.

[0061] The regulatory sequences can be constitutive or inducible. A constitutive regulatory sequence includes CMV (cytomegalovirus), SV40 (Simian virus) and RSV (roussarcoma virus), yeast beta-factor, alcohol oxidase and PGH.

[0062] The regulatory sequences can be inducible which are regulated by environmental stimuli or the growth medium of the cells, including those from the genes for heat shock proteins, alcohol dehydrogenase 2, isocytochrome C,

acid phosphatase, enzymes associated with nitrogen catabolism, and enzymes responsible for maltose and galactose utilization.

[0063] In one embodiment, the cell-specific, upstream regulatory sequence can include a Prostate Specific Antigen (PSA) promoter (Pang, et al., 1995 Hum. Gene Ther. 6:1417-1426; Lee, et al., 1996 Anticancer Res. 16:1805-1811; Martiniello, et al., 1998 Hum. Gene Ther. 9:1617-1626; Pang, et al., 1997 Cancer Research 57:495-499; L Wu, et al., 2001 Gene Therapy 8:1416-1426).

[0064] In another embodiment, the cell-specific regulatory sequence can include a Prostate Specific Cell Antigen (PSCA) promoter (Watabe, et al., 2002 Proc. Natl. Acad. Sci. USA 99:401-406; Bahrenberg, et al., 2001 Cancer Lett. 168:37-43; Jain, A., Lam, A., Carey, M. and Reiter, R. (2002) Identification of an Androgen-Dependent Enhancer Within the Prostate Stem Cell Antigen Gene. *Molecular Endocrinology* 16:2323-2337.).

[0065] In another embodiment, the cell-specific regulatory sequence can include a human Kallikrein 2 (hK2) promoter (Song, et al., 1996 Immunopharmacology 32:105-107; Song, et al., 1997 Human Genet. 99:727-734; Wang, et al., 1997 Immunopharmacology 36:221-227; Chao and Chao 1997 Immunopharmacology 36:229-236; Xiong, et al., 1997 Biochem. J. 325(Pt 1):111-116; Zhang, et al., 1999 Endocrinology 140:1665-1671; Xie, et al., 2001 Hum Gene Ther. 12:549-561).

[0066] The cell-specific, upstream regulatory sequence can be isolated from various organisms including prokaryote or eukaryote organisms, such as bacteria, virus, yeast, plant, insect, or mammal. The mammals include mouse, rat, rabbit, dog, cat, horse, cow, goat, pig, fish, monkey, ape or human. In one embodiment, the upstream regulatory sequence is an intact, human PSA enhancer sequence including nucleotides -5824 through -2855, linked to an intact human PSA promoter sequence including -541 through +12.

[0067] The upstream regulatory sequence is operably linked, to control transcription of the nucleotide sequence encoding a transactivator protein. The transactivator protein includes a DNA-binding domain, linked in-frame, with a transcription activation domain. The DNA-binding domain can include the DNA-binding domain of yeast GAL4, or bacterial LexA. The transcription activation domain can include the transactivator domain of herpes simplex VP-16 (Sadowski, et al., 1988 Nature 335:563-564) or forkhead in rhabdomyosarcoma (FKHR) (Massuda, et al., 1997 Proc. Natl. Acad. Sci. USA 94:14701-14706). Other transcriptional activator domains can be used (Ma and Ptashne 1987 Cell 48:847-853; Ma and Ptashne 1987 Cell 51:113-119; Brent and Ptashne 1985 Cell 43:729-736; Hope and Struhl 1986 Cell 46:885-894 (e.g., GCN4); Gill and Ptashne 1987 Cell 51:121-126). Other transcriptional activator domains include MAPK-responsive ELK-1, steroid receptors, and those from the Ets family.

[0068] In one embodiment, the effector sequence includes between 1 through 4 copies of VP-16. In another embodiment, the nucleotide sequence encoding the transactivator protein includes a DNA-binding domain of yeast GAL4 and between 1 through 4 copies of a transactivator domain of herpes simplex VP-16 (Emami and Carey 1992 The EMBO Journal 11:5005-5012).

[0069] In a preferred embodiment, the effector nucleotide sequence includes: an intact upstream regulatory sequence of a human PSA enhancer sequence including nucleotides -5824 through -2855, linked to an intact human PSA promoter sequence including -541 through +12, operably linked to a nucleotide sequence encoding the transactivator protein includes a DNA-binding domain of yeast GAL4 and a transactivator domain of herpes simplex VP-16.

[0070] In a more preferred embodiment, the effector nucleotide sequence includes: a modified upstream regulatory sequence including two copies of a human PSA enhancer sequence including nucleotides -4326 through -3935 (Pang, et al., 1997 Cancer Res. 57:495-499), with an intervening 890 bp sequence from -3743 through -2855 between the enhancer and promoter deleted, linked to an intact human PSA promoter sequence including -541 through +12, operably linked to a nucleotide sequence encoding the transactivator protein includes a DNA-binding domain of yeast GAL4 (encoding amino acids 1-147) and between 1 through 4 copies of a transactivator domain of herpes simplex VP-16 (encoding amino acids 413-454).

[0071] The most preferred embodiment of the effector nucleotide sequence includes 2 copies of the transactivator domain of VP16, encoding amino acids 413-454.

Reporter Sequences

[0072] The present invention provides reporter nucleotide sequences including 1 through 9 copies of a DNA-binding sequence. In one embodiment, the DNA-binding sequences can be isolated from yeast GAL4 or bacterial LexA or from PAX3 paired box gene 3 (PAX3) (Massuda, et al., 1997 Proc. Natl. Acad. Sci. USA 94:14701-14706). The DNA-binding sequence is linked to a promoter sequence. The promoter sequence can be a minimal promoter sequence. The promoter sequence includes sequences necessary for core promoter function. The promoter sequence can include a TATA box sequence. The promoter sequence can be isolated from any source including bacteria, virus, yeast, plant, insect, or mammal. In particular, the minimal promoter can be isolated from any virus including adenovirus, adenoviral-associated, retrovirus, lentivirus, herpes simplex virus, or retrovirus. In one embodiment, the promoter is isolated from any serotype of adenovirus, including serotypes A through F. In another embodiment, the promoter is isolated from any adenoviral early region, including E1a, E1b, E2a, E2b, E3, and E4. In a preferred embodiment, the promoter includes the TATA box sequence from adenoviral E4 gene.

[0073] In reporter nucleotide sequence invention includes a promoter operably linked to a heterologous nucleotide sequence encoding a heterologous gene product. In one embodiment, the reporter nucleotide sequence includes a minimal promoter operably linked to a chimeric heterologous gene sequence encoding two or more different heterologous gene products. In this embodiment, the different heterologous gene sequences are joined to form a fusion sequence which is operably joined in-frame, or the different heterologous sequences are arranged in a bi-cistronic construct (141-143). Other constructs include a multiple promoter construct where the different heterologous sequences are joined to a different promoter sequence. The reporter nucleotide sequence includes a bi-directional promoter sequence operably linked to two different heterologous gene

sequences (148). Alternatively, two or more different reporter nucleotide sequences can be introduced to a cell, where the different reporter nucleotide sequences comprise a promoter operably linked to a heterologous nucleotide sequence encoding a heterologous gene product.

[0074] The heterologous gene product can encode a reporter gene product, a therapeutic gene product, and/or an immunologically active protein comprising a domain that binds a target.

[0075] The reporter gene product includes proteins that are detectable via various methods including colorimetric, fluorescence, optical, biochemical assays, or radiotracing. The reporter gene sequence can encode beta-galactosidase, luciferase, chloramphenicol acetyl-transferase, dopamine type-2 receptor (D₂R) or mutant forms including D₂R80A and D₂R194A, and somatostatin receptor type-2 (SSTR2), or beta-lactamase. The reporter gene sequence can encode green fluorescent protein (GFP), or derivatives thereof such as YFP (yellow fluorescent protein), CFP (cyan fluorescent protein) or RFP (red fluorescent protein).

[0076] Alternatively, the heterologous gene sequence encodes proteins having therapeutic function such as cytotoxic function. The heterologous gene product having therapeutic function includes, but is not limited to, a toxin, a cytokine, an antibody, lymphokine, oncostatin, enzyme, or an enzyme that converts a prodrug into a cytotoxic drug.

[0077] Examples of therapeutic gene products include, but are not limited to ricin, ricin A-chain, diphtheria toxin, *Pseudomonas* exotoxin (PE) A, PE40, abrin, arbrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstric-tocin, phenomycin, enomycin, curicin, crotin, calicheami-cin, sapaonaria officinalis inhibitor, or maytansinoids.

[0078] Therapeutic gene products which convert a pro-drug into a cytotoxic drug (e.g., pro-drug activating enzymes), including thymidine kinase (Oldfield 1993 Hum. Gene Therapy 4: 39-69). Thymidine kinase converts pro-drugs acyclovir (9-((2-hydroxyethoxy)methyl)guanine)) or its analog ganciclovir (9-((2-hydroxy-1-(hydroxymethyl)-ethoxy)methyl)guanine) into intermediates capable of inhibiting DNA synthesis of a cell. Cells that express thymidine kinase are susceptible to cell killing upon administration of the prodrug.

[0079] Other examples of therapeutic gene products that convert a prodrug into a cytotoxic drug include cytosine deaminase (Huber 1993 Cancer Res. 53: 4619-4626), nitroreductase (Green 1995 British J. Surgery 82: 1546), carboxypeptidase A (Hamstra 1999 Hum. Gene Therapy 10:235-248); linmarase (Cortes 1998 Gene Therapy 5:1499-1507); xanthine-guanine phospho-ribosyltransferase (Mrox 1993 Hum. Gene Therapy 4:589-595); beta-lactamase (Shepard 1991 Bioorg. Med. Chem. Lett. 1:21-26); alkaline phosphatase (Senter 1988 Proc. Natl. Acad. Sci. 85:48424846); carboxypeptidase G2 (Bagshawe 1991 Dis Markers 9:233-238); DT diaphorase (Knox 1993 Cancer Metasta. Rev. 12:195-212); and beta-glucuronidase (Roffler 1991 Biochem. Pharmacol. 42:2062-2065).

[0080] Other examples of pro-drug activating enzymes include mutant forms of the pro-drug activating enzymes. A mutant form of thymidine kinase, HSV1sr-39TK) utilizes ganciclovir and penciclovir substrates effectively than thy-

midine compared to wild type thymidine kinase (Gambhir 2000 Proc. Natl. Acad. Sci. 97:2785-2790).

[0081] The heterologous sequence can be a nucleotide sequence encoding an immunologically active protein comprising a domain capable of binding a target. The immunologically active protein can be a single-chain, immunologically active protein. The domain can include an antigen-binding site of an antibody that binds the target. The protein domain can include at least one complement determining region of an antibody that binds the target.

[0082] The target can be a target protein, a cell-surface antigen, or a cell-surface receptor. For example, the target protein can be tyrosinase, tyrosinase-related protein, albumin, muscle creatinine kinase, myelin basic protein, glial fibrillary acidic protein, NSE, KDR, E-selectin, endoglin, AFP, CEA, erbB2, muc-1 (DF3), ALA, BLG, osteocalcin, SLP1, HRE, Grp78(BIP), L-plastin, and hexokinase II, egr-1, t-PA, mdr-1, hsp70, E2F-1, cycline A, or cdc25C).

[0083] The immunologically active protein can bind to a target protein, including PSA, PSCA, or Kallikrein 2 (hK2).

[0084] The methods for producing the immunologically active proteins of the invention, synthesis of oligonucleotides, PCR, transforming cells, constructing vectors, expression systems, and the like, are well known in the art (Sambrook et al., eds., *Molecular Cloning, A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press (1989); U.S. Pat. No. 5,637,481 issued to Ledbetter et al.).

[0085] The nucleotide sequences encoding the immunologically active protein may be expressed in a variety of systems. An expression vector, encoding the immunologically active protein is introduced (e.g., transformed) into suitable host cells, such as a bacterial cell (Chaudhary et al., 1987 Proc. Natl. Acad. Sci. USA 84:4538-4542; Cohen, 1971 Proc. Natl. Acad. Sci. USA (1972) 69:2110). The expression vector may be introduced into mammalian host cells using DEAE-dextran mediated transfection, calcium phosphate co-precipitation, lipofection, electroporation, protoplast fusion, or other methods known in the art including: lysozyme fusion or erythrocyte fusion, scraping, direct uptake, osmotic or sucrose shock, direct microinjection, indirect microinjection such as via erythrocyte-mediated techniques, and/or by subjecting host cells to electric currents. The above list of transfection techniques is not considered to be exhaustive, as other procedures for introducing genetic information into cells will no doubt be developed.

[0086] The production of the immunologically active protein can be detected using Coomassie stained SDS-PAGE and/or immunoblotting using anti-idiotypic antibodies that bind to the immunologically active protein.

[0087] The heterologous gene product, including the reporter gene product, the therapeutic gene product, or the immunologically active protein, can be joined to a cytotoxic agent thereby forming a conjugated molecule.

[0088] Techniques for conjugating or joining cytotoxic agents to antibodies are well known and can be adapted for joining cytotoxic agents to the heterologous gene products (see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Anti-

bodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982); Vitetta, E. S. et al., 1993, Immunotoxin therapy, in DeVita, Jr., V. T. et al., eds, *Cancer: Principles and Practice of Oncology*, 4th ed., J.B. Lippincott Co., Philadelphia, 2624-2636).

[0089] Examples of cytotoxic agents include, but are not limited to ricin, ricin A-chain, doxorubicin, daunorubicin, taxol, ethiduum bromide, mitomycin, etoposide, teniposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin D, diphtheria toxin, *Pseudomonas* exotoxin (PE) A, PE40, abrin, arbrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crotin, calicheamicin, sapaonaria officinalis inhibitor, maytansinoids, and glucocorticoid and other chemotherapeutic agents, as well as radioisotopes such as ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

[0090] The heterologous gene products, including the reporter gene product, the therapeutic gene product, or the immunologically active protein, can be joined to a detectable label, including a radioisotope, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator or an enzyme.

Recombinant Nucleic Acid Molecules

[0091] Also provided are recombinant DNA molecules that include the effector and/or the reporter nucleic acid molecules of the invention, or a fragment thereof. As used herein, a recombinant DNA molecule is a DNA molecule that has been subjected to molecular manipulation in vitro. Methods for generating rDNA molecules are well known in the art, for example, see Sambrook et al., *Molecular Cloning* (1989). In the preferred recombinant DNA molecules of the present invention, the effector and/or the reporter sequences, or fragments thereof, are operably linked to one or more expression control sequences and/or vector sequences.

Vectors

[0092] The nucleic acid molecules of the invention may be recombinant molecules each comprising the sequence, or portions thereof, of an effector of reporter nucleotide sequence. The term vector includes, but is not limited to, plasmids, cosmids, and phagemids. The effector and reporter nucleotide sequences can be joined to a single vector or to two different vectors. The effector and reporter nucleotide sequences can be arranged in a head-to-head or head-to-tail orientation on a single vector.

[0093] The vector of the invention can be an autonomously replicating vector comprising a replicon that directs the replication of the recombinant DNA within the appropriate host cell. Alternatively, the vector directs integration of the recombinant vector into the host cell. Various viral vectors may be used, such as, for example, a number of well known retroviral and adenoviral vectors (Berkner 1988 *Biotechniques* 6:616-629).

[0094] The vectors include, for example, a vector derived from herpes simplex virus that targets neuronal cells (Battle-

man et al., *J. Neurosci.* 13:941-951 (1993), an immunodeficiency virus that targets hematopoietic cells (Carroll et al., *J. Cell. Biochem.* 17E:241 (1993), and recombinant adeno-associated viral vectors having general or tissue-specific promoters (Lebkowski et al. U.S. Pat. No. 5,354,678). Recombinant adeno-associated viral vectors can be used to integrate the nucleic acid molecules of the invention into the genome of a cell (Lebkowski et al., *Mol. Cell. Biol.* 8:3988-3996 (1988).

[0095] Retroviral vectors can be used to produce the heterologous gene product. These vectors have broad host and cell type ranges, integrate into random sites in the host genome, express genes stably and efficiently, and under most conditions do not kill or obviously damage their host cells.

[0096] Retroviral vectors contain retroviral long terminal repeats (LTRs) and packaging (psi) sequences, as well as plasmid sequences for replication in bacteria and may include other sequences such as the SV40 early promoter and enhancer for potential replication in eukaryotic cells. Much of the rest of the viral genome is removed and replaced with other promoters and heterologous gene sequences. Modified (defective) retroviruses can be made in which at least one of the genes required for replication is replaced by the gene to be transferred. Vectors are packaged as RNA in virus particles following transfection of DNA constructs into packaging cell lines. These include psi2 which produce viral particles that can infect rodent cells and psiAM and PA 12 which produce particles that can infect a broad range of species. Methods of preparation of retroviral vectors have been described (Moolten & Wells, *J. Natl. Cancer Inst.*, 82:297-300 (1990); Wolff et al., *Proc. Natl. Acad. Sci. USA* 84:3344-3348 (1987); Yee et al., *Cold Spring Harbor Symp. on Quant. Biol. Vol. LI*, pp. 1021-1026 (1986); Wolff et al., *Proc. Natl. Acad. Sci. U.S.A.* 84:3344-3348 (1987); Jolly et al., *Meth. in Enzymol.* 149:10-25 (1987); Miller et al., *Mol. Cell. Biol.* 5:431-437 (1985); and Miller, et al., *Mol. Cell. Biol.* 6:2895-2902 (1986) and Eglitis et al., *Biotechniques* 6:608-614 (1988).

[0097] The effector and reporter molecules of the invention can be introduced into herpes viruses (e.g. HSV-1). Herpes viruses are capable of establishing a latent infection and an apparently non-pathogenic relationship with some neural cells.

[0098] Other virus vectors that may be used for gene transfer into cells for treatment of brain tumors include retroviruses such as Moloney murine leukemia virus (MoMuLV); papovaviruses such as JC, SV40, polyoma, adenoviruses; Epstein-Barr Virus (EBV); papilloma viruses, e.g. bovine papilloma virus type I (BPV); paramyxoviruses; vaccinia; rabies and poliovirus and other human and animal viruses.

[0099] The nucleic acid molecules can be introduced into a cell or subject using retroviral vectors, or infectious viral particles, or non-infectious particles (e.g., helper-dependent). The virus vector can be modified so that it maintains the necessary genes, regulatory sequences and packaging signals to synthesize new viral proteins and RNA but lacks genes conferring oncogenic potential.

[0100] In the case of non-infectious viral vectors, a helper virus genome is required to provide the structural genes necessary to encode viral structural proteins. The helper

virus lacks the viral packaging signal required to encapsulate the helper viral RNA into viral particles. Thus, only the helper-dependent viral vector carrying the heterologous gene sequence and a functional packaging signal, but lacking viral structural genes can be incorporated into a virus particle. The helper and helper-dependent vectors are used to infect a target cell and produce no further infectious virus can be produced since there are no viral structural genes provided. Methods for constructing and using viral vectors are well known in the art and reviewed, for example, in Miller and Rosman, *Biotechniques* 7:980-990 (1992) and Davison and Elliot, *Molecular Virology: A Practical Approach* (IRL Press, New York, 1993).

[0101] The viral or other vector can include a constitutive promoter for constitutive transcription of the transactivator sequence. Examples of constitutive promoters include the cytomegalovirus promoter (Boshart, M. et al., 1985 *Cell* 41:521-530). Viral vectors can include tissue-specific or tumor specific transcription or regulatory sequences to regulate the type of cell that expresses the heterologous gene product by incorporating a tissue-specific promoter or enhancer into the vector (Dai et al., *Proc. Natl. Acad. Sci. USA* 89:10892-10895 (1992).

[0102] The preferred vectors permit transcription and translation of the effector and/or reporter sequences in prokaryotic or eukaryotic host cells.

[0103] The efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell system in use (Scharf, D., et al, 1994 *Results Probl. Cell. Differ.* 20:125-62; Bittner, et al., 1987 *Methods in Enzymol.* 153:516-544). The enhancers, transcriptional elements, and initiation codons can be of various origins, both natural and synthetic.

[0104] The vectors having the effector or reporter sequences include expression vectors which are compatible with prokaryotic host cells. Prokaryotic cell expression vectors are well known in the art and are available from several commercial sources. For example, pET vectors (e.g., pET-21, Novagen Corp.), BLUESCRIPT phagemid (Stratagene, LaJolla, Calif.), pSPORT (Gibco BRL, Rockville, Md.), or ptp-lac hybrids for expression in bacterial host cells.

[0105] Alternatively, the vectors having the effector or reporter sequences are expression vectors which are compatible with eukaryotic host cells. The more preferred vectors are those compatible with vertebrate cells. Eukaryotic cell expression vectors are well known in the art and are available from several commercial sources. Typically, such vectors are provided containing convenient restriction sites for insertion of the desired DNA segment. Typical of such vectors are PSVL and pKSV-10 (Pharmacia), pBPV-1/pML2d (International Biotechnologies, Inc.), pTDT1 (ATCC, #31255), and similar eukaryotic expression vectors.

[0106] Methods for generating a recombinant vector including the effector or reporter sequences are well known in the art, and can be found in Maniatis, T., et al., (1989 in: "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) and Ausubel et al. (1989 in: "Current Protocols in Molecular Biology", John Wiley & Sons, New York N.Y.).

[0107] The vector can include at least one selectable marker gene that encodes a gene product that confers drug

resistance such as resistance to kanamycin, neomycin, tetracycline, or ampicillin. The selectable markers can include dihydrofolate reductase or glutamine synthetase. The vector also comprises multiple endonuclease restriction sites that enable convenient insertion of exogenous DNA sequences.

Host-Vector Systems

[0108] The invention further provides a host-vector system comprising a vector, plasmid, phagemid, or cosmid comprising the effector or reporter nucleotide sequence, or a fragment thereof, introduced into a suitable host cell. In one embodiment, the host cell is introduced with a vector comprising both the effector and reporter nucleotide sequences of the invention. In another embodiment, the host cell is introduced with two or more vectors (preferably two) where one vector comprises the effector nucleotide sequences of the invention and another vector comprises the reporter nucleotide sequences of the invention.

[0109] A variety of expression vector/host systems may be utilized to carry and express the effector or reporter sequences. The host-vector system can be used to transcribe and translate express (e.g., produce) the effector transactivator protein or the reporter heterologous gene product. The host cell can be either prokaryotic or eukaryotic. Examples of suitable prokaryotic host cells include bacteria strains from genera such as *Escherichia*, *Bacillus*, *Pseudomonas*, *Streptococcus*, and *Streptomyces*. Examples of suitable eukaryotic host cells include yeast cells, plant cells, or animal cells such as mammalian cells. A preferred embodiment provides a host-vector system comprising the pBCVP2G5-L vector (Example 2) in mammalian cells. A most preferred embodiment provides a host-vector system comprising the pBCVP2G5-L vector (Example 2) in human prostate cancer cells.

[0110] Introduction of the recombinant DNA molecules or vectors of the present invention into an appropriate host cell is accomplished by well known methods that depend on the type of vector used and host system employed. For example, host cells are introduced (e.g., transformed) with nucleic acid molecules by electroporation or salt treatment methods, see for example, Cohen et al., 1972 Proc Acad Sci USA 69:2110; Maniatis, T., et al., 1989 in: "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. Host cells can also be introduced with nucleic acid molecules by various methods, including liposomes, cationic lipid, salt treatment (Graham et al., 1973 Virol 52:456; Wigler et al., 1979 Proc Natl Acad Sci USA 76:1373-76), diethylaminoethyl dextran, or viral infection. Alternatively, particle bombardment can be used to introduce the vectors of the invention into a host cell (Williams et al., Proc. Natl. Acad. Sci. USA 88:2726-2730 (1991)).

[0111] Successfully transformed cells, i.e., cells that harbor the vector of the present invention, can be identified by techniques well known in the art. For example, cells resulting from the introduction of the vector are selected and cloned to produce single colonies. Cells from those colonies are harvested, lysed and their DNA content examined for the presence of the rDNA using a method such as that described by Southern, J Mol Biol (1975) 98:503, or Berent et al., Biotech (1985) 3:208, or the proteins produced from the cell assayed via a biochemical assay or immunological method.

[0112] In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the

effector or reporter nucleotide sequences. The vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), pIN vectors (Van Heeke & Schuster (1989) J Biol Chem 264:5503-5509), and the like. The pGEX vectors (Promega; Madison, Wis.) may also be used to express fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems are designed to include heparin, thrombin or factor XA protease cleavage sites so that the cloned protein of interest can be released from the GST moiety at will.

[0113] In yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as beta-factor, alcohol oxidase and PGH may be used. For reviews, see Ausubel et al (1989 in: "Current Protocols in Molecular Biology", John Wiley & Sons, New York N.Y.) and Grant et al (1987) Methods in Enzymology 153:516-544.

[0114] In cases where plant expression vectors are used, the vectors having the effector or reporter sequences of the invention can include viral promoters such as the 35S and 19S promoters of CaMV (Brisson, et al., (1984) Nature 310:511-514), or the omega leader sequence from TMV (Takamatsu, et al., (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi et al (1984) EMBO J. 3:1671-1680; Broglie et al (1984) Science 224:838-843); or heat shock promoters (Winter J and Sinibaldi R M (1991) Results Probl Cell Differ 17:85-105) can be used. These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. For reviews of such techniques, see Hobbs, S. in: "McGraw Yearbook of Science and Technology" 1992 McGraw Hill New York N.Y., pp 191-196; or Weissbach and Weissbach 1988 in: "Methods for Plant Molecular Biology", Academic Press, New York N.Y., pp 421-463.

[0115] An alternative expression system that can be used to express the effector and reporter sequences is an insect system. In one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) can be used as a vector to express the effector transactivator and reporter heterologous gene product in *Spodoptera frugiperda* cells or in *Trichoplusia larvae*. The effector or reporter sequence can be cloned into a nonessential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the effector or reporter sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses can then be used to infect *S. frugiperda* cells or *Trichoplusia larvae* in which the effector transactivator or the reporter heterologous gene product can be expressed (Smith et al 1983 J Virol 46:584; Engelhard E. K., et al, 1994 Proc Nat Acad Sci 91:3224-7).

[0116] In mammalian host cells, a number of viral-based expression systems can be utilized. In cases where an adenovirus is used as an expression vector, the effector or reporter sequence can be ligated into an adenovirus transcription/translation vector consisting of the late promoter and tripartite leader sequence. Insertion in a nonessential E1

or E3 region of the viral genome results in a viable virus capable of expressing the effector transactivator or the reporter heterologous gene product in infected host cells (Logan and Shenk 1984 *Proc Natl Acad Sci* 81:3655-59). In addition, transcription enhancers, such as the rous sarcoma virus (RSV) enhancer, can be used to increase expression in mammalian host cells.

[0117] The host cell may be isolated from various animal sources including equine, porcine, bovine, murine, canine, feline, or avian. The host cell may also be isolated from any mammalian source including monkey, ape, or human. The host cell may be isolated from various cell or organ sources including blood, prostate, brain, lung, stomach, bladder, pancreas, colon, breast, ovary, uterus, cervix, liver, muscle, skin, or bone.

[0118] In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the protein include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation. Post-translational processing which cleaves a precursor form of a protein (e.g., a prepro protein) may also be important for correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, 293, WI38, etc. have specific cellular machinery and characteristic mechanisms for such post-translational activities and may be chosen to ensure the correct modification and processing of the effector or reporter gene products.

[0119] For long-term, high-yield production of the effector transactivator or the reporter heterologous gene product, stable expression is preferred. For example, cell lines that stably express the effector or the reporter gene product can be transformed using expression vectors that contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells can be grown in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clumps of stably transformed cells can be proliferated using tissue culture techniques appropriate for the cell type used.

[0120] Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M., et al., 1977 *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al., 1980 *Cell* 22:817-23) which can be employed in tk-minus or apt-minus cells, respectively. Also, anti-metabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M., et al., 1980 *Proc Natl Acad Sci* 77:3567-70); npt, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F., et al., 1981 *J. Mol. Biol.* 150:1-14) and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan 1988 *Proc. Natl. Acad. Sci.* 85:8047-51). Recently, the use

of visible markers has gained popularity with such markers as anthocyanins, β -glucuronidase and its substrate, GUS, and luciferase and its substrate, luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A., et al., 1995 *Methods Mol. Biol.* 55:121-131).

Nucleic Acid Molecules

[0121] In its various aspects the present invention provides recombinant nucleic acid molecules, transformed host cells harboring the nucleic acid molecules, generation methods, and assays.

[0122] The nucleic acid molecules of the invention are preferably in isolated form, where the nucleic acid molecules are substantially separated from contaminant nucleic acid molecules having sequences other than the effector or reporter sequences. A skilled artisan can readily employ nucleic acid isolation procedures to obtain isolated effector or reporter sequences, see for example Sambrook et al., in: "Molecular Cloning" (1989). The present invention also provides for isolated effector or reporter sequences generated by recombinant DNA technology or chemical synthesis methods.

[0123] The isolated nucleic acid molecules include DNA, RNA, DNA/RNA hybrids, and related molecules, nucleic acid molecules complementary to the effector or reporter sequences or a portion thereof, and those which hybridize to the effector or reporter sequences. The preferred nucleic acid molecules have nucleotide sequences identical to or nearly identical (e.g., similar) to the nucleotide sequences disclosed herein. Specifically contemplated are DNA, cDNA, RNA, ribozymes, and antisense molecules.

Identical and Variant Sequences

[0124] The present invention provides isolated nucleic acid molecules having a polynucleotide sequence identical or similar to the effector or reporter sequences disclosed herein. Accordingly, the polynucleotide sequences may be identical to a particular effector or reporter sequence. Alternatively, the polynucleotide sequences may be similar to the disclosed sequences.

[0125] One embodiment of the invention provides nucleic acid molecules that exhibit sequence identity or similarity with the effector or reporter nucleotide sequences, such as molecules that have at least 60% to 99.9% sequence similarity and up to 100% sequence identity with the sequences of the invention. A preferred embodiment provides nucleic acid molecules that exhibit between about 75% to 99.9% sequence similarity, a more preferred embodiment provides molecules that have between about 86% to 99.9% sequence similarity, and the most preferred embodiment provides molecules that have 100% sequence identity with the effector or reporter sequences of the invention.

Complementary Sequences

[0126] The invention also provides nucleic acid molecules that are complementary to the effector or reporter sequences of the invention. Complementarity may be full or partial. When it is fully complementary that means complementarity to the entire sequence. When it is partially complementary that means complementarity to only portions of the sequences of the invention.

Nucleotide Sequences which Hybridize

[0127] The present invention further provides nucleotide sequences that selectively hybridize to the effector or reporter nucleotide sequences of the invention under high stringency hybridization conditions. Typically, hybridization under standard high stringency conditions will occur between two complementary nucleic acid molecules that differ in sequence complementarity by about 70% to about 100%. It is readily apparent to one skilled in the art that the high stringency hybridization between nucleic acid molecules depends upon, for example, the degree of identity, the stringency of hybridization, and the length of hybridizing strands. The methods and formulas for conducting high stringency hybridizations are well known in the art, and can be found in, for example, Sambrook, et al., in: "Molecular Cloning" (1989).

[0128] In general, stringent hybridization conditions are those that: (1) employ low ionic strength and high temperature for washing, for example, 0.015M NaCl/0.0015M sodium titrate/0.1% SDS at 50 degrees C.; or (2) employ during hybridization a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42 degrees C.

[0129] Another example of stringent conditions include the use of 50% formamide, 5×SSC (0.75M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5× Denhardt's solution, sonicated salmon sperm DNA (50 mg/ml), 0.1% SDS, and 10% dextran sulfate at 42 degrees C., with washes at 42 degrees C. in 0.2×SSC and 0.1% SDS. A skilled artisan can readily determine and vary the stringency conditions appropriately to obtain a clear and detectable hybridization signal.

Fragments

[0130] The invention further provides nucleic acid molecules having fragments of the effector or reporter sequences of the invention. The size of the fragment will be determined by its intended use. For example, if the fragment is chosen to be used as a nucleic acid probe or PCR primer, then the fragment length is chosen to obtain a relatively small number of false positives during a probing or priming procedure.

[0131] The nucleic acid molecules, fragments thereof, and probes and primers of the present invention are useful for a variety of molecular biology techniques including, for example, hybridization screens of libraries, or detection and quantification of mRNA transcripts as a means for analysis of gene transcription and/or expression. The probes and primers can be DNA, RNA, or derivative molecules including peptide nucleic acids (PNAs). A probe or primer length of at least 15 base pairs is suggested by theoretical and practical considerations (Wallace, B. and Miyada, G. 1987 in: "Oligonucleotide Probes for the Screening of Recombinant DNA Libraries" in: "Methods in Enzymology", 152:432-442, Academic Press).

[0132] Fragments of the effector or reporter sequences that are particularly useful as selective hybridization probes or PCR primers can be readily identified from the effector or reporter nucleotide sequences, using art-known methods. For example, sets of PCR primers that detect a portion of the

effector or reporter transcripts can be made by the PCR method described in U.S. Pat. No. 4,965,188. The probes and primers of this invention can be prepared by methods well known to those skilled in the art (Sambrook, et al. supra). In a preferred embodiment the probes and primers are synthesized by chemical synthesis methods (ed: Gait, M. J. 1984 in: "Oligonucleotide Synthesis", IRL Press, Oxford, England).

[0133] One embodiment of the present invention provides nucleic acid primers that are complementary to effector or reporter sequences, which allow the specific amplification of nucleic acid molecules of the invention or of any specific portions thereof. Another embodiment provides nucleic acid probes that are complementary for selectively or specifically hybridizing to the effector or reporter sequences or to any portion thereof.

Codon Usage Variants

[0134] The present invention provides isolated codon-usage variants that differ from the disclosed effector or reporter nucleotide sequences, yet do not alter the predicted polypeptide sequence or biological activity of the effector gene product (e.g., the transactivator protein) or the reporter gene product (e.g., the heterologous gene product). For example, a number of amino acids are encoded by more than one codon triplet. Codons that specify the same amino acid, or synonyms may occur due to degeneracy in the genetic code. Examples include nucleotide codons CGT, CGG, CGC, and CGA encoding the amino acid, arginine (R); or codons GAT, and GAC encoding the amino acid, aspartic acid (D). Thus, a protein can be encoded by one or more nucleic acid molecules that differ in their specific nucleotide sequence, but still encode protein molecules having identical sequences. The amino acid coding sequence is as follows:

Amino Acid	One		
	Symbol	Symbol	Letter Codons
Alanine	Ala	A	GCU, GCC, GCA, GCG
Cysteine	Cys	C	UGU, UGC
Aspartic Acid	Asp	D	GAU, GAC
Glutamic Acid	Glu	E	GAA, GAG
Phenylalanine	Phe	F	UUU, UUC
Glycine	Gly	G	GGU, GGC, GGA, GGG
Histidine	His	H	CAU, CAC
Isoleucine	Ile	I	AUU, AUC, AUA
Lysine	Lys	K	AAA, AAG
Leucine	Leu	L	UUA, UUG, CUU, CUC, CUA, CUG
Methionine	Met	M	AUG
Asparagine	Asn	N	AAU, AAC
Proline	Pro	P	CCU, CCC, CCA, CCG
Glutamine	Gln	Q	CAA, CAG

-continued

Amino Acid	Symbol	One Symbol Letter	Codons
Arginine	Arg	R	CGU, CGC, CGA, CGG, AGA, AGG
Serine	Ser	S	UCU, UCC, UCA, UCG, AGU, AGC
Threonine	Thr	T	ACU, ACC, ACA, ACG
Valine	Val	V	GUU, GUC, GUA, GUG
Tryptophan	Trp	W	UGG
Tyrosine	Tyr	Y	UAU, UAC

[0135] The codon-usage variants may be generated by recombinant DNA technology. Codons may be selected to optimize the level of production of the effector or reporter transcript, or the effector or reporter gene product in a particular prokaryotic or eukaryotic expression host, in accordance with the frequency of codon utilized by the host cell. Alternative reasons for altering the nucleotide sequence encoding an effector or reporter transcript include the production of RNA transcripts having more desirable properties, such as an extended half-life or increased stability. A multitude of variant effector or reporter nucleotide sequences that encode the respective effector or reporter gene products may be isolated, as a result of the degeneracy of the genetic code. Accordingly, the present invention provides selecting every possible triplet codon to generate every possible combination of nucleotide sequences that encode the disclosed effector or reporter gene products, or that encode the gene products having the biological activity of the effector or reporter gene products. This particular embodiment provides isolated nucleotide sequences that vary from the sequences of the invention, such that each variant nucleotide sequence encodes a polypeptide having sequence identity with the amino acid sequences of the invention.

Derivative Nucleic Acid Molecules

[0136] The nucleic acid molecules of the invention also include derivative nucleic acid molecules which differ from DNA or RNA molecules, and anti-sense molecules. Derivative molecules include peptide nucleic acids (PNAs), and non-nucleic acid molecules including phosphorothioate, phosphotriester, phosphoramidate, and methylphosphonate molecules, that bind to single-stranded DNA or RNA in a base pair-dependent manner (Zamecnik, P. C., et al., 1978 Proc. Natl. Acad. Sci. 75:280284; Goodchild, P. C., et al., 1986 Proc. Natl. Acad. Sci. 83:4143-4146). Peptide nucleic acid molecules comprise a nucleic acid oligomer to which an amino acid residue, such as lysine, and an amino group have been added. These small molecules, also designated anti-gene agents, stop transcript elongation by binding to their complementary (template) strand of nucleic acid (Nielsen, P. E., et al., 1993 Anticancer Drug Des 8:53-63). Reviews of methods for synthesis of DNA, RNA, and their analogues can be found in: "Oligonucleotides and Analogues", eds. F. Eckstein, 1991, IRL Press, New York; "Oligonucleotide Synthesis", ed. M. J. Gait, 1984, IRL Press, Oxford, England. Additionally, methods for antisense RNA technol-

ogy are described in U.S. Pat. Nos. 5,194,428 and 5,110,802. A skilled artisan can readily obtain these classes of nucleic acid molecules using the herein described effector and reporter sequences (see for example "Innovative and Perspectives in Solid Phase Synthesis" (1992) Egholm, et al. pp 325-328 or U.S. Pat. No. 5,539,082).

RNA Molecules

[0137] The present invention provides nucleic acid molecules that encode the effector or reporter gene products. In particular, the RNA molecules of the invention may be isolated full-length or partial-length RNA molecules or RNA oligomers that encode the effector or reporter gene products.

[0138] The RNA molecules of the invention also include antisense RNA molecules, peptide nucleic acids (PNAs), or non-nucleic acid molecules such as phosphorothioate derivatives, that specifically bind in a base-dependent manner to the sense strand of DNA or RNA, having the effector or reporter sequences, in a base-pair manner. A skilled artisan can readily obtain these classes of nucleic acid molecules using the effector or reporter sequences described herein.

Labeled Nucleic Acid Molecules

[0139] Embodiments of the effector or reporter nucleic acid molecules of the invention include DNA and RNA primers, which allow the specific amplification of the effector or reporter sequences, or of any specific parts thereof, and probes that selectively or specifically hybridize to the effector or reporter sequences or to any part thereof. The nucleic acid probes can be labeled with a detectable marker. Examples of a detectable marker include, but are not limited to, a radioisotope, a fluorescent compound, a bioluminescent compound, a chemiluminescent compound, a metal chelator or an enzyme. Technologies for generating labeled DNA and RNA probes are well known, see, for example, Sambrook et al., in "Molecular Cloning" (1989).

Methods for Producing the Heterologous Gene Product

[0140] The present invention provides methods for producing the heterologous gene product. These methods utilize a cell introduced with the effector and reporter nucleic acid molecules of the invention. The cell can be introduced with nucleic acid molecules of the invention inserted into a vector that permits transcription of the effector transactivator and the heterologous gene sequence. The cell, harboring the nucleic acid molecules of the invention, is induced to produce the heterologous gene product. Alternatively, the cell produces the heterologous gene product constitutively. The heterologous gene product, produced by these methods, can be detected and/or imaged in the cell or in the subject.

[0141] In one embodiment, the steps include: introducing a cell with the nucleic acid molecules of the invention; and culturing the introduced cell under conditions suitable for production of the heterologous gene product. The conditions which are suitable for production of the heterologous gene product include contacting the cell with an agent that induces transcription of the effector transactivator. The transcript is translated into the transactivator protein which activates transcription of the reporter nucleic acid molecule and translation of the heterologous gene product.

[0142] The agent includes agents that are capable of causing transcription of the transcription regulatory

sequences in the effector molecule. For example, the inducing agent can be an androgen that mediates transcription of the effector molecule having a prostate-specific or prostate tumor-specific promoter and/or enhancer. The inducing androgen can be natural or synthetic.

[0143] In another embodiment, the methods for producing the heterologous gene product include: introducing the nucleic acid molecules of the invention into a subject under conditions that permit production of the heterologous gene product.

[0144] The nucleic acid molecules are introduced into the subject via various routes, including intravenous, intraperitoneal, intramuscular, intratumoral, intradermal, subcutaneous, and the like. The nucleic acid molecules of the invention can be introduced at a site distal from a target site, such as a tumor. The heterologous gene product produced by the nucleic acid molecules of the invention can migrate to the target site. For example, the nucleic acid molecules of the invention can be introduced into the subject intramuscularly and the heterologous gene product can migrate to the target tumor via the circulatory system. Alternatively, the nucleic acid molecules of the invention can be introduced at the target site, such as in or proximal to the tumor.

[0145] The conditions which are suitable for production of the heterologous gene product include contacting the cell, so introduced, with an agent that induces transcription of the effector transactivator. The transcript is translated into the transactivator protein which activates transcription of the reporter nucleic acid molecule and translation of the heterologous gene product.

[0146] The present invention also provides methods for producing the heterologous gene product which include: implanting a donor cell into a subject under conditions that permit production of the heterologous gene product, where the donor cell harbors the nucleic acid molecules of the invention. The conditions which are suitable for production of the heterologous gene product include contacting the donor cell, so implanted, with an agent that induces transcription of the effector transactivator. The transcript is translated into the transactivator protein which activates transcription of the reporter nucleic acid molecule and translation of the heterologous gene product.

[0147] The donor cells can be introduced into the subject as a cell suspension or as a solid clump of cells. The donor cells can be introduced into the subject via various routes, including intravenous, intraperitoneal, intramuscular, intratumor, intradermal, subcutaneous, and the like. The donor cells can be implanted at a site distal to the target site, such as a tumor. In such cases, the heterologous gene product is produced by the donor cell and can migrate to the target site. For example, the donor cell can be implanted into the subject intramuscularly and the heterologous gene product can migrate to a prostate tumor target site via the circulatory system. Alternatively, the donor cells can be implanted in or proximal to the target site.

[0148] The donor cell can be a cell from a the subject (e.g., autologous cells) or from a different subject (e.g., non-autologous). Donor cells which harbor the molecules of the invention include any cell from a subject, including blood, prostate, brain, lung, stomach, bladder, pancreas, colon, breast, ovary, uterus, cervix, liver, muscle, skin, or bone.

Cells which harbor the molecules of the invention include any cell from any animal including mouse, rat, rabbit, dog, cat, horse, cow, goat, pig, fish, monkey, ape or human. Non-autologous cells such as allogeneic cells also can be used provided they share histocompatibility antigens with the subject to be introduced.

[0149] Methods for preparing donor cells and implanting donor cells harboring recombinant retroviral vectors carrying a heterologous gene sequence have been described (Gage et al., Ch. 86, in: "Progress in Brain Research", Vol. 78, pp. 651-658, 1988; U.S. Pat. No. 5,529,774).

[0150] A variety of methods can be used to introduce the nucleic acid molecules of the invention into a cell, into a subject, or into a donor cell which is implanted into a subject.

[0151] The molecules of the invention can be introduced as naked nucleic acid molecules (with or without a linked vector), liposomes, virus vectors, viruses, or receptor-mediated agents.

[0152] In one embodiment, introduction of naked nucleic acid molecules or liposomes (e.g., cationic) can be used for stable gene transfer of the nucleic acid molecules. The nucleic acid molecules can be introduced into non-dividing or dividing cells in vivo (Ulmer et al., Science 259:1745-1748 (1993)). In addition, the nucleic acid can be transferred into a variety of tissues in vivo using the particle bombardment method (Williams et al., Proc. Natl. Acad. Sci. USA 88:2726-2730 (1991)).

[0153] The nucleic acid molecules can be encapsulated into liposomes using hemagglutinating viruses including the Japan Sendai virus (Z strain). In one embodiment, the nucleic acid molecules are linked to a vector encapsulated into a liposome HVJ construct prior to injection. Alternatively, the liposomes can be produced using Lipofectamine™. The nucleic acid molecules can be introduced into a cell or a subject via viral vectors or viruses. The selection of a viral vector will depend, in part, on the cell type to be targeted. Specialized viral vectors are well known in the art that can target specific cell types.

[0154] The molecules of the invention can be introduced into a cell or a subject using receptor-mediated delivery methods. The nucleic acid molecules of the invention can be complexed with a tissue-specific ligand. The ligand can be an agent that binds a cell receptor. Alternatively, the ligand can be an antibody that binds a cell receptor. The nucleic acid molecules of the invention can be complexed with the ligand by a covalent, or non-covalent link such as a bridging molecule (Curiel et al., Hum. Gene Ther. 3:147-154 (1992); Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)).

Methods for Detecting Production of the Heterologous Gene Product

[0155] The present invention provides methods for detecting the production of the heterologous gene product. The methods of the invention comprise introducing the effector and reporter nucleic acid molecules of the invention into a cell (e.g., transfected cell) under conditions suitable for production of the heterologous gene product; and detection of the heterologous gene product. The detecting methods of the invention are performed using a cultured transfected cell, a cell transfected in a subject, or a donor cell implanted in a subject.

[0156] The heterologous gene product, which is produced by these transfected cells, is detected using non-invasive radionuclide and/or non-radionuclide techniques that permit detection of the location, magnitude and time variation of the heterologous gene product (P. Ray, et al., 2001 *Semin. Nucl. Med.* 31:312-320).

[0157] The detecting step includes non-invasive techniques such as positron emission tomography (e.g., PET) (S. Gambhir, et al., 1999 *Proc. Natl. Acad. Sci. USA* 96:2333-2338; J G Tjuvavej, et al., 1998 *Cancer Res* 58:4333-4341; S R Cherry, et al., 1997 *IEEE Transactions on Nuclear Science* 44:1161-1166; M E Phelps, 1991 *Neurochemical Research* 16:929-994; S R Cherry and S S Gambhir 2001 *Inst. Lab. Anim. Res. J.* 42:219-232), single photon emission computed tomography (J G. Tjuvavej, et al., 1996 *Cancer Res.* 45:4087-4095; K R Zinn, et al., 2000 *J. Nucl. Med.* 41:887-895), cooled charged coupled device (CCD) camera optical imaging (Honigman, et al., 2001 *Mol. Ther.* 4:239-249); magnetic resonance imaging (A H Louie, et al., 2000 *Nat. Biotechnol.* 18:321-325; R. Weissleder, et al., 2000 *Nat. Med.* 6:351-355), bioluminescent optical imaging (P R Contag, et al., 1998 *Nat. Med.* 4:245-247; A Honigman, et al., 2001 *Mol. Ther.* 4:239-249; J C Wu, et al., 2001 *Mol. Ther.* 4:297-306; M Iyer, et al., 2001 *Proc. Natl. Acad. Sci. USA* 98:14595-14600), and fluorescence optical imaging (M Yang, et al., 2001 *Proc. Natl. Acad. Sci. USA* 98:2616-2621).

[0158] The type of non-invasive technique used to detect the heterologous gene product is selected based on the type of gene product produced. For example, bioluminescent optical imaging (P R Contag, et al., 1998 *Nat. Med.* 4:245-247; J C Wu, et al., 2001 *Mol. Ther.* 4:297-306) has been used to detect production of luciferase.

[0159] Alternatively, cooled charge-coupled device camera has been used to detect luciferase in whole animals (A Honigman, et al., 2001 *Mol. Ther.* 4:239-249; M Iyer, et al., 2001 *Proc. Natl. Acad. Sci. USA* 98:14595-14600).

[0160] In other cases, positron emission tomography or micro PET and radiolabeled tracers have been used to detect a thymidine kinase or a mutant version of thymidine kinase, HSV-sr39tk (S R Cherry, et al., 1997 *IEEE Transactions on Nuclear Science* 44:1161-1166; S. Gambhir, et al., 1999 *Proc. Natl. Acad. Sci. USA* 96:2333-2338; S S Gambhir, et al., 1998 *J. Nucl. Med.* 39:2003-2011; D C MacLaren, et al., 1999 *Gene Ther.* 6:785-79; M Iyer, et al., 2001 *J. Nucl. Med.* 42:96-105; S S Gambhir, et al., 2000 *Proc. Natl. Acad. Sci. USA* 97:2785-2790; S S Gambhir, et al., 1999 *Journal of Nuclear Cardiology* 6:219-233).

[0161] Positron emission tomography and radiolabeled spiperone ($\{(3-(2[^{18}\text{F}]\text{-fluorethyl})\text{spiperone (FESP)}\}$) has also been used to detect dopamine type 2 receptor (D_2R) (D C MacLaren, et al., 1998 *Journal of Nuclear Medicine* 39:35P; D C MacLaren, et al., 1999 *Gene Therapy* 6:785-791).

[0162] In one case, production of thymidine kinase and dopamine type 2 receptor have been simultaneously detected using microPET (M. Iyer, et al., 2001 *Journal of Nuclear Medicine* 42:96-105).

[0163] Magnetic resonance spectroscopy has been used to detect production of the pro-drug enzyme cytosine deaminase (L D Stegman, et al., 1999 *Proc. Natl. Acad. Sci. USA* 96:9821-9826; U Haberkorn, et al., 1996 *Journal of Nuclear Medicine* 37:87-94).

[0164] The production of somatostatin receptor subtype II (SSTr2) has been detected using radiolabeled octreotide (B E Rogers, et al., 2000 *Quarterly Journal of Nuclear Medicine* 44:208-223).

[0165] The following examples are intended to illustrate, but not limit, the scope of the invention.

EXAMPLE 1

[0166] The following example provides description of a two-step transcriptional amplification as a method for imaging reporter gene expression using weak promoters.

[0167] Assays for imaging reporter gene expression are very useful for visualizing molecular events in living animals. Non-invasive imaging of reporter gene expression by using radionuclide and non-radionuclide techniques allows the monitoring of the location, magnitude, and time variation of gene expression in living animals and, in some cases, humans. Applications of reporter genes include: (i) optimization of gene therapy vectors that contain a reporter gene, (ii) imaging cell trafficking by marking cells with a reporter gene *ex vivo*, and (iii) monitoring endogenous gene expression through the use of reporter genes coupled to endogenous promoters in transgenic models. All of these applications should benefit from repetitive, noninvasive monitoring of reporter gene expression.

[0168] Methods to image reporter gene expression in living animals include positron emission tomography (PET) (1, 2), single photon emission computed tomography (3, 4), magnetic resonance imaging (5, 6), bioluminescent optical imaging with firefly luciferase (fl) (7-9), and fluorescence optical imaging with green fluorescent protein (10). A detailed review of the different approaches for imaging reporter genes is reported elsewhere (11).

[0169] The cooled charge-coupled device (CCD) camera offers a convenient, cost-effective, and reproducible method to image fl expression in small living animals (7-9). Recently, real-time monitoring of fl reporter gene expression in various tissues has been evaluated in rodents by using a cooled CCD camera (8). In this article, the authors have demonstrated that injection of adenovirus, AdHIV/fl (the fl expression is driven by the HIV-long-terminal repeat promoter) results in fl expression in the region over the testis in male mice. Transgenic mice with the human bone γ -carboxyglutamate protein promoter driving fl led to gene expression in bones and teeth. The use of tissue-specific promoters in these limited applications was possible, but in many applications specific promoters may not lead to sufficient levels of fl expression. In other cases, enhancement of observable signal may benefit from amplification.

[0170] The advantage of PET over optical approaches is the ability to obtain tomographic and quantitative information with high sensitivity. With appropriate corrections for photon attenuation, scatter, and object size, concentrations of radiolabeled tracers can be reliably estimated (12). Furthermore, unlike optical methods, small animal imaging with microPET (13) directly translates to human studies with clinical PET scanners. We have previously developed methods to monitor adenoviral-mediated herpes simplex virus type 1 thymidine kinase (HSV1-tk) expression *in vivo* by using 18 F-labeled acycloguanosine analogs and microPET (1, 14). We have studied cell lines stably transfected ex

vivo with various PET reporter genes and implanted in mice for imaging with microPET (15, 16). We also have validated the use of a mutant HSV1-sr39tk with enhanced imaging sensitivity (17). In our earlier approaches, the expression of the PET reporter gene was driven by relatively strong promoters [e.g., cytomegalovirus (CMV)] that achieve a constitutive, high level of transcription. In many therapeutic applications, targeted approaches to enhance safety and specificity are highly desirable. To this end, transcriptional targeting by using tissue-specific promoters to limit expression of potential cytotoxic transgenes to the tissue of interest has been frequently used (18-20). In applications where a relatively weak, cellular promoter drives the expression of a reporter gene, one has to contend with weaker transcriptional activity that, in turn, limits the ability to image reporter gene expression *in vivo*. In such cases, it is essential to find ways to enhance the transcriptional activity of such promoters. Several potential methods can be used to increase levels of reporter protein. These include (i) increased transcription by using chimeric promoters that retain tissue specificity (20, 21), (ii) enhancement at the posttranscriptional level (22-24), or (iii) transcriptional amplification approaches discussed next.

[0171] One of the amplification approaches referred to as a two-step transcriptional amplification (activation) (TSTA) approach that can potentially be used to augment the transcriptional activity of cellular promoters uses the GAL4-VP16 fusion protein (25, 26) (**FIG. 1**). This approach is also referred to as a recombinant transcriptional activation approach (27). The yeast GAL4 gene expression system is one of the most widely studied eukaryotic transcriptional regulatory systems (28).

[0172] We are presently evaluating methods to non-invasively image reporter gene expression driven by cellular promoters. We chose to evaluate the prostate-specific antigen promoter (named PSE in this article) as it has been well characterized, determined to be tissue-specific, and is expressed after androgen administration in cell culture and *in vivo* (29). In this study, we chose to take advantage of the strong transactivating properties of the GAL4-VP16 fusion protein to achieve prostate-specific amplification by using the PSE promoter to drive expression of fl or HSV1-sr39tk in an LNCaP prostate cancer cell line. We also validated the system for monitoring reporter gene expression in living mice implanted with LNCaP cells transiently expressing fl by using a cooled CCD optical imaging system.

Materials and Methods

TSTA Experimental Strategy

[0173] The HSV1 VP16 immediate early transactivator contains a highly potent activation domain that, when fused to the GAL4 DNA binding domain, elicits a robust response on a GAL4-responsive promoter (referred to as a minimal promoter in this work) bearing multiple tandem copies of the 17 bp near consensus DNA binding site (25, 26). The VP16 activation domain amino acids 411-490 can be subdivided further into N- and C-terminal subdomains. The C-terminal domain is sometimes toxic to cells and elicits a transcriptional inhibitory phenomenon called squelching (30). GAL4-VP16 is a fusion of the N-terminal portion of the VP16 activation domain from amino acids 413-454 and the GAL4 DNA binding domain amino acids 1-147. It is a potent activator that squelches less effectively than the intact activation domain.

Chemicals

[0174] Methyltrienolone (R1881) was purchased from NEN. Tfx-50 transfection reagent and luciferase assay kit were purchased from Promega. D-Luciferin for use with *in vivo* fl imaging was obtained from Xenogen (Alameda, Calif.). [^3H]Penciclovir (17.6 Ci/mmol) was purchased from Moravek Biochemicals (Brea, Calif.). Testosterone pellets (0.007 mg, 6-h release) were obtained from Innovative Research of America. Matrigel was purchased from BD Biosciences (Bedford, Mass.). Cell Culture. The human prostate cancer cells, LNCaP (provided by C. Sawyers, University of California, Los Angeles), were grown in RPMI 1640 supplemented with 10% FBS and 1% penicillin/streptomycin solution. The C6 rat glioma cells were kindly provided by Margaret Black (Washington State University, Pullman) and were grown in deficient DMEM, supplemented with 5% FBS and 1% penicillin/streptomycin/L-glutamine. HeLa cells (American Type Culture Collection) were grown in DMEM with 10% FBS and 1% penicillin/streptomycin.

Construction of Plasmids/Vectors

[0175] The parental construct, PSE, derived from plasmid PSAR2.4k-PCPSA-P-Lux (29), consisted of a 2.4-kb enhancer fragment (-5322 to -2855) and the proximal promoter region from -541 to +12, upstream of an fl reporter gene. PSE was chosen to be the baseline construct because the 2.4-kb enhancer fragment generates the maximal transcriptional and androgen-responsive activity, comparable to the entire 6-kb regulatory region of the prostate-specific antigen gene (20, 31). The construction of PSE plasmid has been described (20). To construct pBS-PSEGAL4VP16, the HindIII to XbaI GAL4VP16 fragment was excised from pSP72-SV40-GAL4VP16 and inserted into PSE plasmid. The minimal promoter, G5E4TATA (G5E4T) contained templates bearing five 17-bp GAL4 binding sites positioned 23 bases from the TATA box of the E4 gene of adenovirus (32). The G5E4T-fl construct was made by PCR amplification of the relevant GAL4 sites and E4TATA from the pGEM3 G5E4T vector by using an upstream primer with a SacI site attached (cccgagctcatttaggtgacactatag) and a downstream primer with a XhoI site attached (ccctcgagacaccacgacacggcacc). The PCR fragments were digested with SacI and XhoI and cloned into the pGL3 basic vector. The G5E4T-sr39tk plasmid was constructed by excising the G5E4T fragment from pSP72-G5E4T-CAT and cloning into pcDNA3.1 vector. The G5E4T sequence was PCR-amplified by using primer pair 5'-gactagatctacagcttgcacgcag-3' and 5'-gactgctagctcgacacg-gcacca-3' and cloned into the BglII/NheI sites upstream of sr39tk in the main vector, pcDNA3.1. For the sake of convenience, PSEGAL4-VP16 is abbreviated as PG, and the re-reporter plasmid G5E4T-fl is abbreviated as L5. The reporter template G5E4T-sr39tk is referred to as T5. The constructs PSE-fl, PSE-HSV1-sr39tk, and SV40-GAL4-VP16 are abbreviated as PL, PT, and SG, respectively.

Cell Transfections and Enzyme Assays

[0176] On day 1, LNCaP cells were plated in 6-well plates in RPMI 1640 containing charcoal-stripped FBS. Transient transfections were performed 24 h later by using Tfx-50 transfection reagent (Promega). Each transfection mix consisted of 0.5 micro grams of the effector and reporter plasmids or reporter plasmid alone. One hour after trans-

fection, methyltrienolone (R1881) in ethanol was added to the medium at a concentration of 1 nM/well, and the cells were incubated for 48 h. For FL activities (fl refers to the gene and FL to the enzyme), the cells were harvested and assayed for FL activity by using the dual-reporter luciferase assay system (Promega) and a luminometer (Lumat 9507, Berthold, Germany) with an integration time of 10 s. LNCaP cells were also transfected by using CMV-fl plasmid (as a positive control). For the TK assay, the cells were harvested 48 h after transfection and assayed for HSV1-sr39TK enzyme activity (tk refers to the gene and TK to the enzyme) as described (14). For androgen inducibility experiments, LNCaP cells were transiently transfected with PG and T5 constructs in the presence of different concentrations of androgen. After 48 h, the cells were assayed for HSV1-sr39TK activity.

In Vivo Optical Imaging of Fl Expression Using a Cooled CCD Camera

[0177] LNCaP cells were transiently transfected with the effector and reporter plasmids or reporter plasmid alone as described earlier. The cells were harvested 48 h after transfection and resuspended in PBS. An aliquot of 1×10^6 cells was mixed with Matrigel and injected i.p. in female nude mice. Five minutes after injection of the cells, the mice were anesthetized (ketaminexylazine, 4:1), and 200 μ l of D-luciferin (15 mg/ml) was injected (i.p.) 10 min before imaging. After the first scan, the mice were s.c. implanted with 0.007-mg sustained release testosterone pellets and imaged again after 24 h and 48 h. A total of five mice were used for the experiment, and one mouse in each group did not receive the androgen pellet.

[0178] The mice were imaged by using a cooled CCD camera (Xenogen IVIS, Alameda, Calif.) with an acquisition time of 5 min. The animals were placed supine in a light-tight chamber, and a gray scale reference image was obtained under low-level illumination. Photons emitted from cells implanted in the mice were collected and integrated for a period of 5 min. Images were obtained by using LIVING IMAGE software (Xenogen) and IGOR IMAGE analysis software (WaveMetrics, Lake Oswego, Oreg.). For quantitation of measured light, regions of interest were drawn over the peritoneal region, and maximum relative light units (RLU) per min were obtained as validated (9).

Results

TSTA System Mediates Prostate-Specific Amplification of Fl Expression in LNCaP Cells and Demonstrates Cell-Type Specificity

[0179] In transient transfection into LNCaP cells, when GAL4-VP16 was placed under the control of the PSE promoter, it activated poorly in the absence of androgen, but the response in the presence of androgen was significantly higher than that observed by using the reporter template alone (L5) (FIG. 2A). The maximal level of fl expression is observed by using five binding sites upstream of the adenovirus E4 promoter (L5) on the reporter template vs. one or two binding sites. The TSTA system-driven amplification of fl expression in the presence of androgen is similar to the SG-activated expression of a GAL4-responsive fl reporter in the absence and presence of androgen stimulation (–L/+L, FIG. 2A). These results validate the concept that the tissue-specific, ligand-responsive PSE promoter could be substi-

tuted for a strong viral one to elicit similar levels of GAL4-VP16 functional activity. When CMV-fl was compared with the TSTA system, the FL activity by using the TSTA system was observed to be 2- to 3-fold lower than that driven by the CMV promoter. A comparison of fl expression by using both the one-step and the TSTA systems reveals a ~50-fold gain ($P < 0.01$) with the TSTA system when compared with the one-step system (FIG. 2A). To determine whether the TSTA system-mediated amplification is restricted to prostate cells alone, we studied the levels of fl expression in two non-prostate cell lines, C6 and HeLa. Firefly luciferase reporter gene expression after androgen administration is minimal in both the cell lines tested, indicating the tissue-specific nature of the PSE promoter (FIG. 2B). The results indicate a strong stimulatory effect on transcription exerted by the GAL4-VP16 fusion protein while maintaining tissue specificity.

TSTA System Mediates Prostate-Specific Amplification of HSV1-sr39tk Expression in LNCaP Cells, Demonstrates Cell-Type Specificity, and Expression Increases with Androgen Dose

[0180] To test the HSV1-sr39tk reporter system, we used the T5 reporter construct with PG for transient transfections in LNCaP cells. The results with HSV1-sr39tk were similar to that observed by using fl. After androgen treatment, HSV1-sr39tk expression mediated by the TSTA system is significantly greater (~24-fold) ($P < 0.01$) when compared with the expression in cells transfected with the reporter template only (T5) (FIG. 3A). Further, the TSTA system-mediated amplification of HSV1-sr39tk expression levels are ~12-fold greater than those driven by PT alone (one-step) (FIG. 3A) in the presence of androgen. Although the gain in amplification for HSV1-sr39tk is lower than fl, it is nevertheless highly significant ($P < 0.01$). To determine whether the TSTA system-mediated reporter gene amplification is cell-type specific, we studied the levels of HSV1-sr39tk expression in two non-prostate cell lines, C6 and HeLa. HSV1-sr39tk expression level after androgen administration is minimal in both the cell lines tested, demonstrating that the TSTA system-mediated activation from the PSE promoter is highly cell-type specific (FIG. 3B). We further evaluated the effects of androgen response in LNCaP cells by using HSV1-sr39tk. In the absence of androgen, HSV1-sr39tk expression levels are similar to the values obtained by using the reporter template alone (minimal). A concentration-dependent increase in HSV1-sr39TK activity is observed with increasing androgen concentration, indicating that androgen treatment greatly enhances the TSTA system-mediated activation from the PSE promoter (FIG. 3C).

TSTA System Mediates Prostate-Specific Amplification of Fl Expression In Vivo

[0181] To further test the utility of the TSTA system in vivo, we injected transiently transfected LNCaP cells (transfected with PG and L5 plasmids, L5 plasmid alone, and PL plasmid) i.p. in female nude mice. Optical CCD imaging of all mice 15 min after injection of transfected LNCaP cells reveals basal levels of fl expression (RLU/min < 100). The mice were scanned again 24 h and 48 h after the implantation of androgen pellets. The results of the 24-h imaging were similar to those observed at 48 h. Forty-eight hours after pellet implantation, the control mice (L5 plasmid alone) again show minimal levels of fl expression (RLU/

min<100) (**FIG. 4A**). In the mice representing the TSTA system, fl expression is observed to be much higher (RLU/min ~500) when compared with the control and the one-step system (RLU/min<100) (**FIG. 4B**). Mice representing the TSTA system that did not receive androgen pellets displayed basal levels of fl expression at 48 h (**FIG. 4A**). This is indicative of the specificity of androgen in activating the PSE promoter in vivo. The results were found to be reproducible between experimental groups. The induction of transcriptional activation upon androgen administration across five mice in each of two groups is illustrated in **FIG. 5**. The TSTA system-mediated amplification in fl expression shows a ~5-fold gain when compared with the one-step system ($P<0.05$). These results demonstrate the ability to image in vivo the expression of fl driven by a weak, tissue-specific promoter in a mammalian system by using the TSTA approach. The TSTA system mediates tissue-specific expression of fl in a mammalian system.

Discussion

[0182] We have previously demonstrated that adenoviral-mediated HSV1-tk expression can be non-invasively imaged by using acycloguanosine analogs and microPET (1, 14). We have been evaluating methods to non-invasively image reporter gene expression driven by weak promoters such as the PSE promoter. Several of the known weak promoters also demonstrate tissue specificity (33). In the present study, we describe a strategy to overcome the weak transcriptional activity of the PSE promoter for use in tissue-specific imaging applications. We used a two-step transcriptional amplification (activation) approach where, in the presence of androgen, a relatively weak PSE promoter activates a GAL4-VP16 fusion protein, which, in turn, drives reporter gene expression under the control of GAL4 response elements in a minimal promoter.

[0183] In the present study, we observed the TSTA system-mediated amplification of fl expression to be 50-fold higher than the one-step system in LNCaP cells in the presence of androgen. We have also demonstrated the TSTA system to be highly tissue-specific. Similar results were obtained when we changed the reporter gene from fl to the HSV1-sr39tk, although the fold gain in HSV1-sr39tk expression levels was lower than fl. The differences in degree of amplification between fl and HSV1-sr39tk may be attributed to different levels of mRNA amplification and differences in the two enzymes to act on their corresponding substrates. The TSTA system, however, does lead to a statistically significant increase in amplification for both the fl and HSV1-sr39tk in a tissue-specific manner.

[0184] The TSTA system-mediated activation of the PSE promoter depends highly on the levels of androgen as evidenced by the dose-dependent increase in HSV1-sr39tk expression. The system seems to function in a continuous manner (as opposed to a binary on/off fashion). There also does not seem to be a threshold effect. As more androgen becomes available, levels of GAL4-VP16 fusion protein increase, thereby increasing the ability to bind to GAL4 binding sites on the reporter template, resulting in greater levels of fl and therefore greater imaging signal. Finally, although we did not see full saturation, higher levels of GAL4-VP16 have previously been reported to inhibit transcription (referred to as squelching) (30, 34, 35).

[0185] We further tested the utility of the GAL4-VP16 induction system in vivo to non-invasively image tissue-

specific amplification of reporter gene expression. To validate this system in vivo, several issues needed consideration. These included the development of (i) LNCaP and non-prostate cell lines stably expressing both the effector and reporter constructs and (ii) construction of adenoviral vectors containing the two components of the TSTA system. Both of these approaches require considerable time before they can be tested in vivo. To expedite the process of in vivo evaluation, we injected transiently transfected LNCaP cells (using fl as the reporter gene in the absence of androgen) in female nude mice. The mice were imaged by using a sensitive cooled CCD camera before and after implantation of testosterone pellets. All mice displayed basal levels of fl expression in the absence of androgen. Twenty-four to 48 h after androgen administration, the mice representing the TSTA system showed a significantly greater level of fl expression when compared with the control and one-step mice. We observed similar high levels of induction across several mice with a ~5-fold gain for the TSTA system over the one-step system. In fact, in the absence of the TSTA system, the fl expression was close to background, and therefore cells could not be imaged. These initial results are aimed at non-invasively imaging reporter gene expression in a mammalian system by augmenting the transcriptional activity of a weak promoter by using the TSTA system. The level of TSTA amplification in vivo depends on the pharmacokinetics of androgen availability to cells, and it is possible that the in vivo signal can potentially be higher than observed based on the imaging time after androgen induction. Future studies will need to address the exact correlation between levels of androgen in blood and the levels of induction in vivo.

[0186] Fang et al. (36) have examined the functionality of the GAL4-VP16 transactivator to evaluate phosphoglycerate kinase (PGK) promoter activities in vivo by using adenoviral vectors. Nettelbeck et al. (33) have used recombinant transcriptional activation to establish a positive feedback loop initiated by transcriptional activation from a von Willibrand factor promoter. The GAL4-VP16 fusion protein was used to achieve target gene amplification from a prostate-specific antigen promoter (37). Both of these approaches were targeted at increasing the expression of transgenes for use in cancer gene therapy protocols. Further, the GAL4-VP16 responsive TSTA system has been recently used in conjunction with zebrafish tissue-specific promoters with green fluorescent protein reporters (35). In this study, the GAL4-VP16 was injected transiently into fish embryos that developed with minimal toxicity, permitting imaging of specific tissue in adult fish.

[0187] It is important that any reporter gene-imaging approach not significantly perturb the cells/animal models being studied. There is potential for the GAL4-VP16 system to be toxic to cells (35, 38). In zebrafish, low levels of injected GAL4-VP16 were apparently not deleterious to development, whereas higher levels were (35). However, in the current study, only transiently transfected cells were used, so toxicity is not practical to detect. Future studies with stable cell lines, gene therapy vectors, and transgenic animal models will require strict characterization of potential toxicities of the TSTA approach. It may be the case that levels of GAL4-VP16 will need to be modulated to strike a balance between amplification and any potential toxicity.

[0188] The approaches validated in the current study should lead to better vectors for imaging gene therapy, study of tumor growth and regression following pharmacological intervention, as well as development of transgenic models with enhanced reporter gene expression. Applications and extensions of the TSTA approach include: (i) imaging PET reporter genes (e.g., HSV1-sr39tk) and other in vivo reporter genes; (ii) enhancing reporter gene expression by modifying the regulatory components of the PSE promoter and building a single vector that incorporates both components of the TSTA system; (iii) replacement of the PSE promoter with other weak promoters, thereby enabling one to target site-specific genes in vivo; (iv) the study of multiple endogenous genes by driving expression of GAL-4-A from one promoter and B-VP-16 from a separate promoter where genes A and B can be chosen so that their respective proteins interact (this procedure should allow the expression of a reporter gene if and only if both promoters are activated); (v) imaging of protein-protein interactions in vivo using inducible two-hybrid mammalian expression systems; and (vi) amplification of both therapeutic and reporter genes by modifying the reporter template.

EXAMPLE 2

[0189] The following provides descriptions of molecular engineering of a two-step transcription amplification (TSTA) system for transgene delivery in prostate cancer.

[0190] The concept of tissue specific gene therapy and imaging has been hampered by lack of specificity, borderline efficacy and inadequate delivery methods. Improvements in all three areas must occur to translate the promise of gene therapy into meaningful clinical applications [39]. In prostate cancer, the most common strategy to control specificity of transgene expression is to employ the regulatory region of a prostate gene product such as the prostate specific antigen (PSA) (reviewed in [40]). In order to achieve optimal therapeutic efficacy, one goal of the field has been to achieve prostate specific promoter activities similar in magnitude to those of ubiquitously active viral enhancers such as Simian Virus 40 (SV40) and Cytomegalovirus (CMV) [41]. A logical and systematic approach to improve the PSA regulatory regions for combating prostate cancer involves several steps. Novel promoter constructs are engineered and their activity in cell-based transfection studies is evaluated. The most promising constructs are cloned into recombinant adenoviral vectors or other efficient in vivo gene delivery vehicles) and tested in pre-clinical models [42, 43].

[0191] Our labs have recently initiated such studies for prostate cancer. We initially reported a strategy to augment the specificity and activity of the PSA enhancer by exploiting the synergistic nature of androgen receptor (AR) action. The key regulatory elements of the PSA enhancer include a proximal promoter (−541 to +12) comprising two binding sites for the androgen receptor (AREI and II) and a distal enhancer, which contains a 390-bp androgen-responsive core region [44, 45]. The core region contains a cluster of closely spaced androgen response elements (AREs) and sites for other transcription factors [46, 44, 47, 45, 48, 49]. The enhancer is active in both androgen-dependant (AD) and androgen independent (AI) cancer cells [49]. AR binds cooperatively to the enhancer and mediates synergistic transcription [48]. Other factors within and outside of the enhancer contribute to prostate specificity [50-52, 49]. We

found that molecular engineering of the PSA enhancer by duplication of the core or fusion to multiple AREs generated 20-fold higher activities than the parental constructs yet retained androgen inducibility and tissue specificity [53]. Furthermore, we showed that the enhanced activity, inducibility and specificity of the chimeric constructs were maintained in an adenoviral vector expressing firefly luciferase (FL) [53].

[0192] The two-step transcriptional activation system (TSTA) is another strategy for augmenting PSA transgene expression [54]. In the TSTA system, a potent transcriptional activator, which is driven by a cell-specific promoter, acts on a second expression plasmid, which encodes the reporter/therapeutic protein. This two-step approach results in cell-specific amplification of expression. The activator is often GAL4-VP16, a fusion protein comprising the DNA binding domain from the yeast transcription activator GAL4 and the activation domain from the Herpes Simplex Virus 1 activator VP16. GAL4-VP16 assumes a unique specificity and potency that does not naturally exist in the mammalian cells [55, 56]. The cell specific TSTA approach is based on the original “enhancer trap” methodology employed in *Drosophila* to study developmental regulation of gene expression [57, 58].

[0193] In one application of the TSTA approach to prostate cancer, Segawa and colleagues attached the 5.3-kb intact PSA regulatory region to GAL4-VP16 and demonstrated androgen-dependant activation of a FL reporter gene bearing upstream GAL4 binding sites and ablation of cancer cells using a TSTA-driven toxic gene [59]. Our groups employed a similar TSTA expression approach but coupled it to imaging of prostate cancer in living mice. Prostate cancer cells injected into live mice were visualized using a cooled Charge Coupled Device (CCD) optical imaging camera by using a streamlined 2.4-kb PSA enhancer-promoter attached to a FL reporter, [60]. In both cases, the TSTA system maintained androgen responsiveness, yet substantially amplified the signal versus the reporters driven directly by the PSA regulatory region.

[0194] In the current study, we sought to optimize the TSTA system for molecular imaging with eventual applications to therapy. Noninvasive molecular imaging with reporter genes can be used for imaging tumors and metastases, to monitor the therapeutic efficacy of drugs, cell trafficking, gene delivery and expression, as well as the study of various transgenic models [61]. Our objective was to augment the promoter activity and generate a titratable system. Augmented activity will be required to transition the FL-based CCD approach to clinically relevant methodologies such as positron emission tomography (PET). Titratability of expression, on the other hand, is an important safeguard in gene therapy. Often, the untoward side effects of introducing and expressing exogenous genes in animals and patients can not be fully predicted by in vitro or tissue culture experimentation. In addition, titratability is necessary because tumors and cell lines display varying AR responses [62, 63]. For example, biphasic effects of androgen on AR activity have been observed and excess levels of androgen inhibit PSA production and cell growth [64]. A study on the LNCaP subline also suggests that chronic androgen treatment induces reversible cell adaptation to the stimulant [65]. An additional complexity is that excess GAL4-VP16 exhibits a transcriptional inhibitory effect

called squelching [66], which can generate cell toxicity and might confound TSTA under certain conditions (see, for example, [67]).

[0195] The concept of adjusting transgene expression by controlling the activator and promoter potency is detailed in older studies by one of us on GAL4-derived activators [56]. In a subsequent study, a wide range of activities was generated by exploiting the synergistic behavior observed by varying the number of activation domains on the GAL4-derived activator and GAL4 binding sites on the reporter plasmid [68]. Here we combine the modified GAL4 system with natural and chimeric PSA enhancers to create a highly active, robust expression system for prostate cancer gene imaging and therapy. We demonstrate the cell specificity, efficacy and utility of this system by imaging living mice using cooled CCD optical technology.

Results

The Chimeric TSTA System

[0196] We outline the TSTA rationale in **FIG. 6A**. There are four primary variables in our system: i. The potency of the prostate specific promoter driving GAL4-VP16 (the effector) (**FIG. 6B**); ii. the number of GAL4 binding sites proximal to the FL reporter gene (**FIG. 6C**); iii. the potency of the GAL4-VP16 derivative (**FIG. 6B**); and iv. The presence of the effector and reporter genes on the same plasmid (**FIG. 6D**). Each variable offers a unique opportunity to modulate gene expression.

[0197] We employed two variants of the tissue specific PSA promoter (**FIG. 6B**). The first is PSE, which contains a 2.4 kb fragment (−5824 to −2855), encompassing the 390 bp core PSA enhancer core region (−4326 to −3935), linked to the proximal PSA promoter (−541 to +12). The second, PSE-BC ([53], abbreviated as PBC here), contains the PSA enhancer with a duplicated 390-bp core but a deletion of an 890 bp intervening sequence between the enhancer and promoter (−3743 to −2855). These modifications augmented androgen-responsive expression 20-fold in cell culture [53].

[0198] The reporter templates contain the FL gene under the control of 1, 2 or 5 copies of the 17 bp GAL4 binding sites positioned 23 bp upstream of a minimal promoter containing the adenovirus E4 gene TATA box (**FIG. 6C**) [68]. The resulting plasmids are termed G1-L, G2-L and G5-L. We used PSE and PBC to express recombinant GAL4-VP16 variants to generate a series of effector plasmids that display a gradient of activities (**FIG. 6B**). PSE expresses the 147 amino acid GAL4 DNA binding domain (DBD) bearing a single copy of the 42 amino acid VP16 activation subdomain (amino acids 413-454), PSE-VP1 [68]. We engineered PBC to express GAL4 DBD fusion proteins containing 1, 2 or 4 copies of the VP16 subdomain. We abbreviated the resultant plasmids as PSE-VP1, PBC-VP1, PBC-VP2 and PBC-VP4 and cloned the optimal combination of PBC-VP2 and G5-L into a single plasmid termed PBCVP2G5-L.

[0199] We expressed the parental plasmids GAL4-VP1, -VP2 and -VP4 from the SV40 enhancer as positive controls to provide a benchmark for comparison. As an additional benchmark, we used a FL construct driven by the CMV enhancer termed CMV-L. We systematically evaluated the TSTA constructs by co-transfection assays into the androgen-responsive prostate cancer cell line, LNCaP, in the

presence of 10 nM R1881. We normalized each experiment using either CMV-L or the SV40 constructs and graphed representative individual experiments. Subsequently, we tested several cell lines to evaluate cell specificity. For ease of comparison with the TSTA system, we will refer to PSE or PBC directly driving FL expression as the one-step system.

Evaluation of the Variables

[0200] We evaluated the variables to determine i. the relative efficacies of the one-versus the two-step systems; ii. the use of PSE versus PBC to drive GAL4-VP16 expression; iii. the effect of varying the number of GAL4 binding sites; and iv. the effect of varying the number of VP16 activation domains.

[0201] The TSTA system displayed enhanced activity and androgen inducibility versus the one-step system in transfection assays. Co-transfection of PSE-VP1 and G5-L resulted in an activated level in cell culture that was 250-fold greater than the PSE-L one-step construct (**FIG. 7**). Further, the TSTA system retained strong androgen-responsiveness (compare + and −R1881). However, the PBC-VP1/G5-L combination exhibited an induced activity only 15-fold better than the PBC-L. Comparison of PSE-VP1 and PBC-VP1 on G5-L revealed only a 1.5-fold difference, which is not considered significant ($P=0.1$). This value was much less than the 20-fold difference observed between PSE-L and PBC-L [15] suggesting that despite the augmented potency of PBC, the FL levels in LNCaP cells begin to saturate with G5-L as a reporter.

[0202] Variation of the number of GAL4 binding sites contributed to the titratability (**FIG. 8**). The activity with PSE-VP1 increased nearly 8 fold after increasing the number of sites from one (G1-L) to two (G2-L). However, raising the number of sites from two (G2-L) to five (G5-L) increased the activity an additional 60-fold. The pattern changed when examining the combination of a stronger promoter, PBC, and a more potent activator, GAL4-VP4. In this example, the largest increase in activity, 30-fold was observed from G1-L to G2-L. From G2-L to G5-L there was only a 15-fold increase. The activity appears to saturate at five GAL4 sites because G9-L exhibited the same activity as G5-L with PBC-VP2 as an effector. In summary, PSE-VP1 and PBC-VP4 both increase transcription activation synergistically as the number of activator binding sites increases. The magnitude of the synergy and the absolute level of activation, however, are related to the potency of the effector plasmid, providing a strategy to further adjust the expression levels in this system.

[0203] The final parameter we measured was the effect of multimerizing the VP16 activation domain (**FIG. 9**). With G5-L as reporter, PBC-VP2 displayed a 3-fold greater activity than PBC-VP1 ($P=0.0007$). Surprisingly, PBC-VP2 is modestly better than PBC-VP4 ($P=0.02$), possibly because PBC-VP4 is causing an inhibitory phenomenon called squelching [66]). Nevertheless, the hallmark was the combination of PBC-VP2 and G5-L, where the level of activated expression reproducibly exceeded the activity of both benchmarks (CMV-L and the combination of SV40-VP4 with G5-L). **FIG. 10** illustrates the full spectrum of expression levels observed in our system, with an 800-fold variation from the weakest one-step to the strongest two-step system.

Tissue/cell Specificity of the TSTA System

[0204] We chose the TSTA combination of PBC-VP2 and G5-L for analysis of tissue specificity (**FIG. 11**). We compared prostate and non-prostate lines, and cell lines expressing and lacking AR to assess authentic prostate specificity and distinguish it from simple androgen responsiveness. The LAPC4 cell line is an advanced prostate cancer cell (tumor cells from patient with refractory/metastatic prostate cancer) line that expresses AR and displays modest androgen-responsiveness as measured by PSA induction [69]. The mammary carcinoma cell line MCF-7 also expresses AR but not PSA. The human cervical cancer cell line HeLa cell is negative for AR and PSA. fAR-HeLa expresses flag-tagged human AR but not PSA [48]. Finally, we included the human hepatic cell line HepG to test for potential activity in liver.

[0205] During our initial tests we discovered that CMV-L responds to androgen stimulation (**FIG. 9**). We employed SV40-driven GAL4-VP2 and G5-L as a benchmark to properly normalize experiments in different cell types. The SV40-VP2/G5-L displayed a similar activity as CMV-L in LNCaP and was not significantly affected by androgen in any cell lines tested. In LNCaP cells, we consistently observed that, in the presence of androgen, the combination of PBC-VP2 and G5-L had an activity that was similar to that of SV40-VP2 and G5-L. This observation was consistent with immunoblotting results (**FIG. 11**, panel B) where PBC and SV40 expressed GAL4-VP2 at similar levels. However, PBC expression was androgen-dependent whereas SV40 expression was not influenced by androgen.

[0206] As shown in **FIG. 11** we found that the TSTA system displayed activities comparable to the SV40 benchmark only in the prostate cancer cell lines, LNCaP and LAPC4 (>90% and 75%, respectively). In contrast, we found that the activities of the TSTA system relative to the benchmark were 0.2% in HepG cells, 0.7% in HeLa cells and 1.5% in MCF-7 cells. In a system where AR was overexpressed, fAR-HeLa cells, the TSTA system elicited 2% the activity of our benchmark. The difference between HeLa and fAR HeLa was significant ($P=0.4$).

The Effector and Reporter on the Same Plasmid

[0207] A single plasmid bearing both the effector and reporter greatly increased activity but maintained cell selectivity (**FIG. 12**). The construct, referred to as PBCVP2G5-L, contains a 3.5-kb PBC-VP2 NotI fragment inserted into the G5-L (**FIG. 6D**) in a "head to head" orientation, with 170-bp between G5 and the 5' end of the distal copy of the PSA core enhancer. Transfection of the single construct PBCVP2G5-L into LNCaP cells yielded an activated FL activity 10-fold higher than that seen with the same molar amount of the two-construct PBC-VP2/G5-L TSTA system. The single construct did not display as much activity relative to the benchmark in LAPC4 cells, possibly due to the reduced androgen dependency of LAPC4. Nevertheless, PBCVP2G5-L maintained tissue selectivity as illustrated by its low activity in HeLa, fAR-HeLa, HepG2, and MCF7 cells. When we cloned the PBC-VP2 NotI fragment in the "head-to-tail" orientation with G5-L to generate a single construct, we discovered that PBCVP2G5-L(R) displayed greatly reduced activity versus the head-to head orientation. We do not understand the cause of this effect.

Application of the Chimeric-TSTA System to Imaging FL Reporter Gene Expression in Living Mice

[0208] We show that the chimeric-TSTA system displays robust expression in imaging studies in live mice. To validate the potential of the modified TSTA for imaging we determined whether the differences in activity could be reproduced qualitatively in an animal imaging system. A cooled charge coupled device (CCD) camera converts bioluminescent photons to quantifiable electronic signals. The luminescence is recorded and graphically displayed by superimposing a colored topographic pseudoinage on a photograph of the animal. Previous studies had established that within the proper time frame, the RLU signals acquired by the camera are linear to exposure time and amount of FL activity as assayed by luminometry [70]. We transfected LNCaP cells or HeLa cells with our optimal TSTA constructs, treated with R1881, and implanted the cells subcutaneously onto the dorsal surface of the mice. We separated the mice into 4 groups. Within each group we injected three types of transfected cells. To eliminate positional artifacts, we performed the experiments in triplicate; we rotated each group of cells through all three implantation sites. **FIG. 13** shows pictures of representative mice from each group. In group 1 (**FIG. 13A**), the G5-L negative control showed no detectable signal and the signal generated by PSE-L was barely above the background. In contrast the signal for the one-step vector PBC-L was evident and equal to 800 RLU/min at the maximum intensity. When we analyzed the two-step system (**FIG. 13B**), signals of over 6500 RLU/min were obtained with the optimal two-construct TSTA system.

[0209] The signals appeared to be both ligand- and cell-specific. HeLa cells transfected with PBC-VP2/G5-luc (**FIG. 13C**), or LNCaP cells grown without R1881 did not display a signal above background. Remarkably, we estimated the maximum signal from PBCVP2G5-L, the single construct, to be 55,000 RLU/min, which is nearly 10-fold greater than the signal generated by the two-construct TSTA system (**FIG. 13C**). CMV-luc exhibited a similar signal in both LNCaP and HeLa cells. In summary, we have presented here our initial effort to apply the augmented TSTA system to molecular imaging and we discuss the potential applications of this system below.

Discussion

Use of the Chimeric TSTA System to Modulate Expression

[0210] We have modulated the activity of the TSTA system by introducing potent PSA enhancers and potent derivatives of GAL4-VP16. Remarkably, the largest increases in activity came not from increasing the potency of the PSA promoter but from either increasing the potency of the activator or by placing the TSTA components on a single plasmid. As shown in **FIG. 8**, increasing the number of activator binding sites from G1 to G5 greatly amplifies the activity by 240 to 450 fold, depending on the activator expressed (PSE-VP1 or PBC-VP4). Moreover, duplication of the activation domain from PBC-VP1 to PBC-VP2 resulted in a 3-fold enhancement of activity. These results reinforce the concept of synergistic activation of transcription and its use in varying the activity of an expression system.

[0211] We observed the single most dramatic increase in activity by placing the TSTA system on a single plasmid.

Comparison in LNCaP cells of the single construct, PBCVP2G5-L, with the combination, PBC-VP2 and G5-L, revealed a striking 10-fold difference. The positioning of the two components on the same DNA molecule may generate a feed forward loop, where GAL4-VP16 drives G5-L and raises its own expression level by binding upstream of PBC. Similar loops have been described [71]

[0212] There are numerous combinations that could still be tested. The effects of the PSE-VP2 or -VP4 series have not been compared with PBC-VP2 and -VP4. Additionally, certain conditions, such as the R1881 concentration, have not been adjusted; this was performed in an earlier study [60]. However, the values will likely fall within the ranges we observed. The study has indicated that we have reached, or are close to, the limit of amplification using the present TSTA components.

[0213] Others have explored the concept of TSTA in imaging and gene therapy. The Fraser group used a TSTA system, which employed a GFP effector, and achieved enhanced, tissue specific bioluminescent signals to study Zebra fish development [67]. Segawa and colleagues combined the PSA wild type enhancer-promoter with GAL4-VP16 for gene therapy in prostate cancer [59] and our groups recently employed an early version of TSTA in imaging.

[0214] Remarkable progress has been reported by others, who have explored the optimization of prostate specific promoters. For example, the prostate specific PSA and human Kallikrein 2 (hK2) promoter/enhancers have been modified to generate potent androgen-responsive expression systems analogous to our chimeric enhancers [72, 73]. A direct comparison of the studies is difficult because of differences in enhancers, reporters (GFP vs. FL), minimal promoters, positive benchmarks (different CMV constructs) or methods of DNA transduction. We emphasize that our study was geared towards the same endpoint as the others but we focused on increasing potency and signal flexibility for use in imaging and therapy. By employing transient transfection assays we demonstrated the amplitude, titratability and specificity of our system over an 800-fold range. We tested certain points within this range and they maintained the same approximate activities by a cooled CCD imaging approach. The strongest constructs repeatedly exceeded the activities of multiple benchmarks.

Activity, Inducibility and Specificity

[0215] The current methodology prohibits us from drawing conclusions about the absolute degree of androgen inducibility. Basal expression increased as the activity of the system increased from the one-step to the most potent two-step constructs. We believe that much of the increase in basal expression is a consequence of incomplete depletion of steroids from the cultured cells. The argument is based on two observations: i. The basal activity of the PSA enhancer constructs in charcoal-stripped serum can be further reduced by addition of the anti-androgen casodex. ii. The small amount of residual androgen in charcoal-stripped medium will likely result in the same amount of activator being synthesized when comparing different GAL4-VP16 derivatives expressed from a similar promoter such as PBC. This point is supported by our result showing that the 3-fold increase in potency of activators, i.e., PBC-VP1 vs. PBC-VP2, is observed both in the presence and absence of R1881.

Nevertheless, the system still displayed cell type specificity. Ultimately, the most rigorous test of true androgen responsiveness and tissue specific expression will be to perform transgenic animal studies or to employ viruses stably expressing the TSTA system to infect xenografts or other animal models; this is the current focus of our research.

Applications to In Vivo Imaging

[0216] The cooled CCD optical imaging belongs to a new generation of in vivo imaging technologies that use fluorescent or bioluminescent reporter genes to produce a signal from within a living animal. The CCD approach detects low levels of luminescence consistently and reproducibly from fur-covered animals without the need for an external light source. [74, 70].

[0217] Luciferase monitoring of transgene expression is still in its infancy and is limited to small animals due to significant absorption and scatter of visible light within the animal [70]. Positron emission tomography (PET) is a technology currently employed in clinical settings [75-77]. PET utilizes molecular probes labeled with positron emitting isotopes and produces dynamic signals measurable by a circular array of detectors. PET generates tomographic images reflecting the concentration and location(s) of probes in a living subject of any size. Successful PET imaging has been performed with the Herpes Simplex-Virus-1 (HSV-1) Thymidine Kinase (TK) reporter gene expressed from a CMV enhancer [75, 77]. TK utilizes ¹⁸F-labeled ganciclovir/penciclovir to generate a signal primarily in cells expressing the reporter gene. However, for some applications PET may have a lower sensitivity than bioluminescence imaging [70]. A significant improvement in sensitivity, in order to image the least number of cells, is necessary to make reporter gene-based PET methods viable for imaging prostate cancer progression in pre-clinical and clinical models. The modifications reported in our current system are aimed at improving a prostate-specific PET-based reporter gene methodology.

Extensions of the TSTA System

[0218] The TSTA system can be manipulated for use in targeting cancer in different ways. New cell and promoter specific regulatory elements can be introduced to further up- or down-regulate expression [54]. Replacement of the VP16 activation domain with domains responsive to unique signals can be employed to identify novel cellular signaling pathways. Furthermore, other prostate cancer promoters can be utilized and novel reporter or therapeutic genes can be added. These additions will increase the utility and regulatability of TSTA. Although androgen and AR are central to early prostate cancer progression, later stages of proliferation gradually utilize cross-talk among AR and signaling cascades including MAPK, PI3K, PKA, EGFR, IGFR and TGF- β [78, 79, 69, 80, 81]. The concept of TSTA can be readily applied to understanding the ramifications and activity of these cellular pathways during cancer progression.

[0219] In conclusion the major advances of TSTA are its cell selectivity, activity and robustness relative to cell specific promoters. Its flexibility will permit widespread utility in cancer research.

Materials and Methods

Cell Culture

[0220] We grew the human prostate cancer cell line LNCaP in RPMI 1640 supplemented with 10% Fetal Bovine Serum and 1% Penicillin/Streptomycin solution. We grew HeLa, FAR-HeLa [48], and the human hepatic line HepG cells (ATCC) in DMEM with 10% Fetal Bovine Serum and 1% Penicillin/Streptomycin. We grew the human prostate cancer line LAPC4 [69] in IMDM (GIBCO) with 10% Fetal Bovine Serum and 1% Penicillin/Streptomycin. Prior to transfection, we transferred the cells for 24 hours into media that contains 5% charcoal stripped serum.

Plasmids

[0221] The baseline PSA promoter construct termed PSE and the chimeric PSE-BC (abbreviated here as PBC) are as previously described [53]. To construct pPSE-VP1, the HindIII-XbaI fragment was excised from pSV40-VP1 and inserted downstream of the 2.4 Kb PSA promoter PSE. We generated the other effectors, PBC-VP1, PBC-VP2 and PBC-VP4 using similar strategies [53]. We constructed G1, G2 and G5-L as described [60]. We cloned the NotI Fragment bearing the PBC promoter and GAL4-VP2 gene into the NotI site of G5-L generating a single vector termed PBCVP2G5-L that contained both components of the TSTA system.

Cell Transfection

[0222] On day 1, we plated LNCaP cells in 6-well plates in RPMI 1640 containing charcoal stripped FBS. We performed transient transfections 24 hours later using Tfx-50 (Promega) with a lipid:DNA ratio of 4:1. Each transfection mixture contained 0.5 µg of the effector and reporter plasmids or reporter plasmid alone with pGL3B carrier DNA. Methylenetriethanolamine (R1881; NEN Life Science Products, Boston, Mass.) was added to the medium at a concentration of 10 nM/well one hour following transfection, and the cells were incubated for 48 h. The cells were harvested and lysed using the passive lysis buffer provided in the assay kit for measuring FL activities (Dual-Reporter Luciferase Assay System, Promega). FL activities of 5% of the cell lysates with 100 ml of substrate D luciferin were measured using a luminometer (Lumat 9507, Berthod Germany) with an integration time of 10 sec.

Immunoblot Analysis of GAL4-VP16 Expression

[0223] LNCaP cells were grown in 10-cm dishes and transfected with select plasmids expressing the TSTA components. We harvested and lysed the treated cells using RIPA lysis buffer (10 mM Tris-HCl, 150 mM NaCl, 0.1% SDS, 1% DOC, 1 mM EDTA and 1% NP40). We normalized extracts by protein concentration (Bio-Rad Dc protein assay Kit), the samples were fractionated on 4-15% gradient acrylamide gels (Bio-Rad) and subjected to immunoblot analysis with rabbit polyclonal antibodies generated against intact GAL4-VP16 [82].

In Vivo Studies

[0224] We treated transiently transfected LNCaP and HeLa cells with 10 mM R1881, harvested 40 hours post-transfection and resuspended in phosphate buffered saline (PBS). We anesthetized female nu/nu mice with 40 µl of ketamine-xylazine (4:1) solution. To allow time for tissue

distribution, a solution of D-luciferin (Xenogen, CA) in PBS (200 ml, 15 mg/ml) was injected into the peritoneal cavity prior to implanting cells. After 5 min, 1×10^6 cells were suspended in 50 µl PBS, combined with 50 µl of Matrigel (BD Biosciences, Bedford Mass.) and injected subcutaneously onto the dorsal side of the mice. Each mouse bore injections at 3 sites. Twenty minutes after intra-peritoneal injection of D-luciferin, we imaged the mice using a cooled CCD camera (Xenogen IVIS, Xenogen Corp., Alameda, Calif.). At the time of injection into animals, an aliquot of the cells was also analyzed for FL activity using a luminometer as described above. All studies were performed with full approval from the UCLA Animal Research Committee (ARC).

CCD Imaging and Quantitation

[0225] We placed the mice prone in a light-tight chamber and a gray scale reference photograph was obtained under low-level illumination. We collected photons emitted from within the mouse and transmitted through tissue and integrated them for an acquisition time of 1 to 5 min. We obtained images and analyzed them using Living Image Software v4.02 A (Xenogen Corporation, Alameda, Calif.) v2.11 and Igor Image Analysis Software Wavemetrics, Seattle, Wash.). We drew regions of interest (ROI) over the visible light signal to quantitate the light. We normalized the maximum relative light unit (RLU) signals measured to acquisition time to obtain maximum (RLU/min). We calibrated the system as described earlier [70].

EXAMPLE 3

[0226] The following provides descriptions of visualization of advanced human prostate cancer lesions in living mice by a targeted gene transfer vector and optical imaging.

[0227] Continued improvements in screening, early detection, and treatment of localized disease have led to a steady decline in prostate cancer mortality over the past ten years (83-85). Despite these advancements, prostate cancer continues to be the second highest cause of cancer deaths in American men. Endocrine therapy, employing castration and/or anti-androgens, is the only effective treatment for advanced, metastatic disease (86, 87). Even though these patients continue endocrine therapy, prostate cancers invariably relapse within a mean time of 18-36 months (88), after which they are considered androgen-independent (AI), and are unresponsive to existing treatments. Vector-based prostate delivery of therapeutic transgenes represents a potential alternative or adjuvant to existing therapies, such as chemotherapy or radiotherapy, for the treatment of AI disease. As with other emerging therapies, vector-based approaches are challenged with achieving acceptable levels of efficacy and safety. Use of strong constitutive viral promoters, such as those of cytomegalovirus (CMV) and Rous sarcoma virus (RSV), enables high levels of therapeutic transgene expression, but could result in accompanying damage to healthy tissues (89). To improve the activity and specificity of prostate-targeted gene expression, we recently developed enhanced promoters designed to augment prostate-specific transgene expression by multimerizing key regulatory elements in the prostate-specific antigen (PSA) enhancer and promoter (90). One such promoter, PSE-BC, was 20-fold more active than the native PSA enhancer/promoter in cell-based firefly luciferase expression studies. Furthermore,

when incorporated into an adenovirus vector (AdPSE-BC-luc), the promoter exhibited greatly enhanced transcriptional activity in LNCaP prostate cancer cells and restricted transgene expression in several non-prostate cell lines and mouse tissues (90).

[0228] To further advance the concept of prostate-targeted expression, we tested our approaches in several recently developed human prostate cancer (CaP) xenograft models, designated the Los Angeles Prostate Cancer (LAPC) series, which was derived from clinical tissues obtained from patients with advanced CaP and grafted into severe combined immune deficient (SCID) mice. The models retain characteristics of clinical disease, including androgen receptor (AR) and PSA expression, the requirement for androgens, and metastatic potential (91, 92). One of the models, LAPC-4, initially requires androgen for growth, but similar to clinical disease progression, tumors regress upon castration and an AI tumor emerges (91). Demonstration of the utility of our approaches in clinically relevant models suggests that they may be applicable in clinical settings.

[0229] The application of a non-invasive imaging modality in a CaP-targeted gene therapy model may greatly aid in accurate assessment of in vivo vector-mediated gene transduction and therapeutic efficacy. The recently developed cooled charged coupled device (CCD) camera for optical imaging is a sensitive approach for detecting bioluminescence emitted from luciferin reacting with firefly luciferase in living animals (93-95). The advantages of a targeted gene transfer approach coupled with non-invasive imaging include the ability to localize diseased tissue, and importantly, to accurately monitor the kinetics and levels of transgene expression in diseased and healthy tissues. In this study, we employed CCD imaging to achieve those ends in several mouse models of human CaP.

Results

Discriminatory Expression Capability of a Prostate Specific Gene Delivery Vector

[0230] We first assessed the in vivo transcriptional targeting capability of AdPSE-BC-luc in comparison to the strong constitutive AdCMV-luc (94). After systemic tail vein injection of either Ad, luciferase expression was monitored. The CCD signals are dependent on the administration of D-luciferin substrate, as omission of luciferin results in weak background signals (FIG. 14A). The magnitudes of light signals (maximum relative light units, RLU) are linearly proportional to the image acquisition time (94). This important feature of cooled CCD camera allows the signal intensity to be normalized to the acquisition time and be reported as maximum RLU/min, represented by the color scale. The acquisition times were reduced to offset strong signal intensities that saturate the CCD camera (e.g., liver signal in CMV cohorts; FIG. 14A). Despite comparable gene delivery to the liver in both groups (FIG. 14B), AdPSE-BC-luc-mediated expression in the liver was less than 10^{-5} that of AdCMV-luc, as measured by CCD imaging and luminometry of tissue extracts from isolated livers (FIG. 14A and Table 1). These data confirmed that AdPSE-BC-luc has high specificity for prostate tissue (90), as indicated by its poor expression in liver, the major site of expression for AdCMV-luc. Furthermore, this non-invasive imaging modality correlates well with current in vitro biochemical analysis of luciferase activity (94).

[0231] The prostate-specific transcriptional activity of AdPSE-BC-luc was evaluated by direct injection of Ad into several human CaP tumors implanted into murine subcutaneous tissues in the lower back. The results from AD LAPC-4 models are shown in FIG. 15. The activity of AdPSE-BC-luc in LAPC-9 tumors was similar to that observed in LAPC-4. Based on the activity seen 8 days post-injection, AdPSE-BC-luc displayed 72-fold lower expression in AD LAPC-4 tumors than AdCMV-luc (FIG. 15 and Table 1). By comparing the ratio of activity in LAPC-4 tumors to that in livers, AdPSE-BC-luc exhibited ~1000 fold higher preferential expression in CaP tumors than AdCMV-luc (FIGS. 14 and 15, and Table 1).

Kinetics of Transgene Expression in Living Mice Bearing Human Prostate Tumors

[0232] One major advantage of the CCD non-invasive imaging system is the ability for repetitive monitoring of Ad-based luciferase gene transfer and expression in the same animal over time. Because the experiment was carried out entirely in the same animal, and without any variation in the genetic background or in gene delivery, smaller study cohorts could be used. Luciferase expression was evaluated in mice bearing AD LAPC-4 tumors spanning a 3-week period after intra-tumoral injections of AdCMV-luc (FIG. 15A) or AdPSE-BC-luc (FIG. 15B). The intra-tumoral signals in the AdCMV-luc injected mouse (CMV1) displayed the highest activity between 2 and 4 days post-injection, and diminished thereafter (FIG. 15A). Leakage of AdCMV-luc into the circulation after intra-tumoral injections was observed in LAPC-4 tumors, as indicated by the signals appearing in the liver (FIG. 15A). In fact, after 4 days, the liver signals exceeded those in the tumor, and gradually increased over time (FIG. 15A and Table 1). The intra-tumoral signals continued to decrease to a level below the minimum scale of 1×10^5 RLU/min at 15 days post-injection, whereas the liver signal remained robust at $\sim 1.5 \times 10^6$ RLU/min in this animal (CMV1).

[0233] By comparison with Ad-CMV-luc, the time course of intra-tumoral AdPSE-BC-luc expression was delayed (FIGS. 15A and 15B). The majority of the AdPSE-BC-luc injected tumors expressed negligible luciferase at 2 days post-injection (3/5 mice). All 5 mice in the cohort start to display signals at 4 days, and peaked signals between 8 to 11 days post-injection (FIG. 15B and Table 1). The delayed course of Ad-PSE-BC-luc-mediated expression may be attributed to its lower transcriptional activity relative to AdCMV-luc. In the AdPSE-BC-luc-injected cohort of 5 mice, only signals emitted from the tumors were detected at time points on or before 15 days post-injection (FIG. 15B). However, at 21 days post-injection, low-magnitude extra-tumoral signals were visible (FIG. 15B) in 3 out of 5 animals. These low-magnitude signals (~ 200 RLU/min; FIG. 15B) were distinguishable from background luminescence because CCD imaging of the same animal at 2 days post-injection, a time point just prior to initiation of expression, revealed the background to be ≤ 70 RLU/min. To localize the origin of light emission, we isolated organs from the BC4 mouse and re-imaged at the time of sacrifice (FIG. 15C). The signals in the upper chest and lower back emanated from the animal's lung and spine, respectively (FIGS. 15B and 15C).

Detection and Localization of Human Prostate Cancer Metastatic Lesions

[0234] We undertook detailed histological evaluation of the isolated organs to determine whether metastatic lesions were in fact detected by our methodology. The elongated spinal signal was well-localized within the length of the spinal column (**FIG. 15C**), so we processed this specimen for further histological and immunohistochemical analysis. Higher magnifications revealed a large, elongated metastatic lesion embedded in spinal musculature, characterized by large pleomorphic nuclei and a high mitotic rate consistent with neoplasia (**FIGS. 16A and 16B**). Immunohistochemistry performed with an anti-human pan-cytokeratin antibody confirmed that the lesion was of human origin (**FIGS. 16A and 16B**). The spinal lesion of another animal in the cohort (BC2) also demonstrated the same histological characteristics and a clear correspondence of CCD signal and lesion location at the caudal end of the spine (**FIG. 16B**). In another animal with lung signals (**FIG. 16C**), we processed the lung for immunofluorescent evaluation by confocal microscopy, using the human cytokeratin antibody. Evaluation of lung sections revealed specific cytoplasmic localization of the human pan-cytokeratin antibody, which was identical to that seen in cells of the xenograft and metastatic spinal lesion (**FIG. 16C**). The staining was undetectable in the lungs of non-tumor-bearing mice used as negative controls. Tumor cells in the lung were detected as micrometastatic nodules of 9 to 74 cells in several independent locations that occupied $377 \mu\text{m}^3$ of the right lung and $46 \mu\text{m}^3$ of the left lung. The predominant localization of micrometastasis in the right lung of this animal corresponded well with the CCD imaging result (**FIG. 16C**).

Elevated PSA-Based Expression in Advanced Androgen Independent Tumors

[0235] To determine whether AdPSE-BC-luc would be active in AI tumors grown in the absence of testicular androgen, we first evaluated whether there were obvious differences between either endogenous AR or PSA expression in the AD and AI LAPC-4 xenografts. This result would offer insights regarding the expression of the exogenously introduced luciferase gene. **FIG. 17A** shows that neither protein is down-regulated in AD and AI tumors. In contrast, PSA protein expression appeared to increase in the AI subline. This up-regulated endogenous PSA expression paralleled the exogenously introduced luciferase expression mediated by AdPSE-BC-luc (**FIG. 17B** and Table 1). The CCD images of 3 animals from both AD and AI LAPC-4 tumor-bearing cohorts, 11 days after intratumoral injection, are shown in **FIG. 17B**. At this time point, 9.8-fold higher activity was observed in AI as compared to AD tumors (**FIG. 17B** and Table 1). Uneven vector distribution and gene transfer are known to occur in intra-tumoral injections¹⁴. To rule out this limitation as a reason for higher gene expression in AI versus AD tumors, we performed ex vivo infection of single-cell suspensions derived from the AD and AI xenografts. Both CaP tumor cell types were easily infected by Ads, but there was higher luciferase expression in AI than in AD LAPC-4 tumor cells (**FIG. 17C**).

Discussion

[0236] Hormone therapy for prostate cancer has changed little since its introduction 30 years ago, yet it continues to be the only effective treatment for advanced disease (97). As

a result, gene-based therapeutic strategies, covering a broad spectrum of approaches, have emerged as promising alternatives or adjuvant to existing modalities, including replacement of defective tumor suppressors, cytotoxic enzyme-prodrug therapy (suicide gene therapy), suppression of tumor-angiogenesis, and up-regulation of immune-mediated tumor surveillance (98). However, the design and application of vector-based cancer gene therapies must address issues of both efficacy and safety.

[0237] Efficacy in vector-based gene therapy is dependent in part on the ability of a vector to infect and transduce cells of the target tissue. Our results demonstrate that our prostate-specific Ad was capable of transducing both the AD LAPC-4 and LAPC-9 prostate cancer xenografts. This study also showed that as LAPC-4 tumors progressed from AD to AI, the AI tumor cells continued to express AR, PSA, and the luciferase gene, despite the complete absence of testicular androgen (**FIG. 17**). Remarkably, not only was the PSA-based Ad transcriptionally active in AI prostate tumors, it displayed nearly 10-fold higher activity than in AD LAPC-4 tumors. As all of the models retain important features of advanced clinical disease (91, 92), these data support the possibility that a prostate-specific vector capable of transducing prostate cells in human patients can be developed to treat advanced disease.

[0238] One interesting observation that we noted in the AR immunohistochemical analysis was that positive AR staining appeared to be more diffuse and less nuclear localized in the AI than in AD tumor sections (**FIG. 17A**). This observation is consistent with our current understanding that nuclear translocation of AR is mediated in part by androgen binding to the receptor (99). When testicular androgen is depleted as in the LAPC-4 AI model, AR nuclear translocation is impeded but not completely inhibited (**FIG. 17A**). Both the mechanism of AR translocation and the functional role of nuclear localized AR in this setting may be key to understanding transcriptional regulation in AI prostate cancer cells. Due to the largely qualitative nature of immunohistochemical analysis we need to fully characterize the AR localization and functional activity in the LAPC-4 model at the molecular level. However, many studies provide evidence that AR can function in AI disease. The evidence includes AR mutations that confer expanded ligand specificity (100), AR gene amplification and over-expression (101), cross-talk between other signaling cascades and AR pathways (102, 103) and increased expression of the nuclear receptor transcriptional co-activator, TIF2 (104). In fact, over-expression of Her-2/neu has been implicated in AI progression of both the LAPC-4 model (103) and clinical cases (105). Regardless of the precise mechanism(s), a better understanding of the critical transcriptional regulatory pathways operative in advanced AI prostate cancer should enable the development of even more effective approaches for targeting this disease in the future.

[0239] One prominent, serendipitous discovery that arose from our study was detection of metastatic lesions. Although the precise transduction mechanism of the metastatic lesions is unclear at this time, we postulated that intra-tumoral injection of AdPSE-BC-luc leaked to the systemic circulation, in a route similar to the case in AdCMV-luc, and infected metastatic lesions. No discernable liver signal was detected in the AdPSE-BC-luc cohorts, because the tissue specificity of the PSE-BC promoter prevented expression in

the liver. This hypothesis is supported by our recent preliminary results showing that metastatic lesions can be detected by systemic tail vein injection of AdPSE-BC-luc. The alternative explanation for detecting metastasis could be the dissemination of a transduced cell(s) from the primary tumor. This hypothesis is less likely, especially in the case of the large spinal lesions (**FIGS. 16A and 16B**), because Ad-mediated expression is known to be transient, and expansion from a single cell to the large lesion would likely have resulted in loss of expression. However, lung micrometastases could have originated from transduced cancer cells in the xenografts.

[0240] Although CCD imaging can sensitively and specifically monitor luciferase expression in small animal models, it lacks the ability to provide detailed tomographic information (93-95). On the other hand, Positron Emission Tomography (PET) is a clinically utilized imaging modality that can provide quantitative, three-dimensional localization of imaging signals. In fact, we have demonstrated that high-resolution micro-positron emission tomography (microPET) can track Ad mediated herpes simplex virus thymidine kinase gene expression in the livers (106) and tumors (96) of living mice. Currently, studies to optimize parameters of imaging of PET reporter transgene in human volunteers have been initiated (107). In preparation for the transition to clinical applications, it will be important to validate our vector-mediated cancer targeting approaches utilizing microPET in animal models. Appropriate resolution of the issues discussed should continue to improve the design, efficacy, and safety of prostate cancer gene-based diagnostic and therapeutic strategies.

Methods

Mice and LAPC Xenograft Propagation

[0241] SCID (scid/scid) mice were bred and maintained as previously described (91). Male mice of approximately 3 months of age were utilized in our studies. Mice were anesthetized as described (94) for all surgical or imaging procedures. LAPC-4 and LAPC-9 seed tumor cells from frozen stocks were generously provided by Dr. Charles Sawyers (91, 92). Xenografts were initiated by implanting ~10⁶ viable cells subcutaneously with Matrigel (Collaborative Biotech Products, Bedford, Mass.), 50:50 by volume totaling 100 μ l. Once tumors were established, further expansion and propagation of tumors were accomplished by implanting tumor fragments of 1-2 mm³, and the AI sublines were grown and passaged several rounds in surgically castrated male mice (91). The viral injections were performed when the tumors reached a diameter of ~5-7 mm, which required about 3-4 weeks of tumor growth from the initial time of tumor passage. Single cell suspension transient cultures of xenografts were generated as described (92).

Adenoviral Vectors and Southern Hybridization

[0242] AdCMV-luc and AdPSE-BC-luc were generated as previously described (90, 94). The Ads were titered by plaque assays on 293 monolayer cells (i.e. infectious units=plaque forming units). Total cellular DNA was extracted from the livers of two treatment cohorts at 4 days post Ad injection. The Southern blot conditions were as previously described (90). The liver tissues were homogenized and lysed by proteinase K, and total DNA was purified by phenol/chloroform extraction, followed by ethanol precipi-

tion. DNA was digested with Not I, subjected to agarose gel electrophoresis. NotI restriction digestion liberated a 2.8 kb CMV-luc and a 4.6 kb PSE-BC-luc expression cassette. Non-radioactive digoxigenin (Roche Co. Germany) labeled luciferase DNA fragment was used as probe (90).

CCD Imaging to Detect In Vivo Luciferase Expression

[0243] The same total dose of 1.8×10^9 infectious units were injected either systemically via tail vein or intra-tumorally. For intra-tumoral injections, Ad were given in 6 doses of 10 μ l each into 3 sites on 2 consecutive days. The procedures for animal imaging studies were performed as described (94). At the specified days post-injection, the CCD images were acquired using the Xenogen In Vivo Imaging System (Xenogen IVISTM, Alameda Calif.), adapted with a cooled CCD camera. Image analysis was performed using IGOR software (Wavemetrics, Lake Oswego, Oreg.). The increase in RLU is linearly proportional to the increase in acquisition time (94). Therefore, we normalized the signal intensity to the image acquisition time (RLU/min), such that an expanded range of comparative values beyond the saturation limit of 65,000 maximum RLU could be achieved. The image analysis software can quantify signal intensities by integrating over a region of interest (ROI) represented by RLU/pixel/min. We found, however, that due to the great range of signal intensities and light deflection properties, the pixel values can vary significantly, depending on the ROI region drawn. This limitation makes comparison between different experimental conditions difficult. Thus, we used the maximum RLU/min within a ROI, not integrated over the pixels, as the unit to compare the CCD signals, and the results correlated very well with luminometer readings of tissue extracts (Table I) (90, 94).

Confocal Microscopy Study of Lung Metastasis

[0244] Mice with signal in the lungs were evaluated by confocal microscopy to determine whether the signal from the reporter gene reflected metastatic events. Animals were perfused with 2% paraformaldehyde, and lungs were inflated with 3% agarose. Specimens were subsequently fixed by immersion in the same fixative, washed in PBS, and embedded on 7% agarose. Fragments from the tumor were used as positive control. Sections of 500 μ m were obtained with a vibrotome, and stained with human-specific anti-keratin antibody (AM273-5M, BioGenex, San Ramon, Calif.) and a CY3-conjugated secondary antibody. Observation was performed on a confocal microscope (BioRad 1024 confocal microscope, Hercules, Calif.), and ImagePro4.0 software was used for quantification of serial sections.

Immunohistochemical Analysis of Tumor Sections

[0245] Immunohistochemistry was performed according to Leav et al. (108). Briefly, tissue sections were deparaffinized, and antigen retrieval was achieved by boiling in 0.1M sodium citrate pH 6.0 for 15 min. Tissue sections were incubated at 4 degrees C. overnight with respective antibodies, alpha-cytokeratin cocktail AM273-5M (BioGenex, San Ramon, Calif.), AR-beta 5 micro g/ml (UpState, Lake Placid, N.Y.), or PSA 1:40 (Novocastra, Ontario L7N 3J5, Canada). Stringent blocking and washing procedures were carried out to reduce background staining, prior to adding multilink 1:20 (BioGenex, San Ramon, Calif.) and AP label 1:20 at room temperature for 20 min each. Finally, sections

were washed again before color development with DAB (BioGenex, San Ramon, Calif.). The micrographs were visualized with an Olympus BX41 microscope, and images captured by an Olympus Camedia C-3030 digital camera.

TABLE 1

Table 1. Summary of CCD image signal intensities and luminometry results of luciferase expression in mice.						
Systemic Injections						
Naive Animals a	days p.i.	CMV	(n)	PSE-BC	(n)	CMV/PSE-BC b
Max. CCD Imaging Signal (RLU/min) in liver						
	4	7.6E+7	7	402	7	1.9E+5
	11	6.0E+7	3	952	3	6.3E+4
Luminometry Readings (RLU/ug protein), liver						
	4	2.2E+7	5	70	5	3.1E+5
Intra-tumoral injections						
Max. CCD Imaging Signal (RLU/min) in tumor (T) or liver (L)						
LAPC-4 (AD)	days p.i.	CMV (L)	(n)	CMV (T)	PSE-BC (T)	CMV/PSE-BC b
	4	3.3E+5	3	7.2E+4	3	897
	8	1.1E+6	3	4.3E+4	3	1798
	11	c		4.2E+4	3	1309
	15	1.0E+6	3	d		1237
	21	6.7E+5	3	d		1311
LAPC-4 (AI)	days p.i.		PSE-BC	(n)		AI/AD e
	4		925	3		1
	8		8586	4		4.8
	11		12803	4		9.8
	15		7498	4		6.1
	21		3291	4		2.5

a Non-tumor bearing, naïve mice.

b Calculated by dividing average signals in the AdCMV-luc-treated group by the respective signals in the AdPSE-BC-luc-treated group.

c Incomplete data collected for this time point.

d Unable to determine. Due to the dominant signals in the liver, the signals in the tumors were below the minimum image analysis setting used.

e Calculated by dividing the average signals for the AI LAPC-4 cohort by the signals for the AD LAPC-4 cohort at the same time point post-injection.

EXAMPLE 4

[0246] The following example provides description of monitoring gene therapy with reporter gene imaging.

[0247] Advent of new techniques in molecular biology and their integration into nuclear medicine provides a great opportunity to improve the quality of diagnosis and treatment of many diseases. Methods are actively being developed for controlled gene delivery to various somatic tissues, including tumors, using novel formulations of DNA and for controlling gene expression using cell specific, replication-activated, and drug-controlled expression systems (109-111). Although various methods of gene therapy have met with very limited success, it is likely that eventually many disease processes will be successfully treated with delivery of one or more genes to target tissue(s). A major concern for the application of gene therapy is to achieve a controlled and effective delivery of genes to target cells and to avoid expression in non-target locations. Imaging the expression of a particular therapeutic gene is likely to be critical to

optimizing gene therapy. Direct imaging of the expression of every therapeutic gene would require development of hundreds of different radiolabeled probes targeted against each therapeutic protein, and thus the development of a more general approach to indirectly monitor therapeutic gene expression is needed. The reporter gene approach is one such potential approach that has been well validated in pre-clinical models and is the focus of the current review.

Reporter Gene Concept

[0248] Reporter genes have long been used to study various aspects of gene expression including, promoter/regulatory elements, inducible promoters and endogenous gene expression (112, 113). The general concept is that regulatory regions of genes (e.g., promoters/enhancers) can be cloned and used to drive transcription (the process of converting DNA to mRNA) of a reporter gene. By introducing a reporter gene driven by a promoter of choice into target tissue(s), one can indirectly monitor expression of the gene whose promoter has been cloned. This avoids having to build a specific probe to evaluate the expression of every new gene. The use of a promoter of choice also allows expression of the reporter gene only in select tissues, because specific promoters are active only in specific tissues. Conventional methods used by molecular biologists to monitor gene expression take advantage of reporter genes like β -galactosidase (114, 115) and chloramphenicol-acetyltransferase (CAT) (116, 117), which require tissue samples for determining their expression levels. Other methods make use of optical reporter genes such as luciferase (118, 119), green fluorescent protein (GFP) (120-122) or β -lactamase (123). The optical reporter genes have been used in living animal models as well but are not generalizable for human applications (124).

[0249] Due to technological innovations (125, 126) such as positron emission tomography (PET) and single photon emission computed tomography (SPECT), it is now possible, using radiotracers (reporter probes), to image reporter gene expression in vivo both repeatedly and non-invasively. Radiotracer imaging techniques offer the ability to monitor the detailed location, magnitude and time-variation of reporter gene expression.

Adapting the Reporter Gene Concept for Radionuclide Imaging

[0250] In order to adapt the reporter gene concept for imaging with PET or SPECT two primary approaches are possible (FIG. 18). The reporter gene can be chosen so that it encodes for an enzyme that is capable of trapping a tracer by action of the enzyme on a chosen tracer. A second approach uses a reporter gene that encodes for an intracellular and/or extracellular receptor capable of binding a tracer (e.g., radioactive ligand). The accumulation of the tracer in both approaches is dependent on the expression of the reporter gene. Through the choice of the right tracer and optimization of its pharmacokinetics it is possible to primarily achieve imaging signal only in those areas in which the reporter gene is expressed. The introduced reporter gene driven by a promoter of choice is sometimes referred to as a transgene. This reporter gene-imaging paradigm is independent of a particular delivery vector; it can be used with any of the several currently available vectors (e.g., retrovirus, adenovirus, adeno-associated virus, lentivirus, liposomes, etc.). The common feature for all vectors is the

cDNA expression cassette containing the reporter gene(s) of interest. The promoter can be constitutive, leading to continuous transcription, or can be inducible leading to controlled expression. The promoter can also be cell specific, allowing expression of the reporter gene to be restricted to certain cells.

[0251] The ideal reporter gene would have the following characteristics: (A) When expressed, the reporter gene protein should produce specific reporter probe accumulation only in the cells in which it is expressed. (B) When the reporter gene is not expressed, there should be no accumulation of the reporter probe in cells. (C) There should be no immune response to the reporter gene product and this product should not significantly perturb the cell. Other desirable characteristics are also important and are reviewed elsewhere (127).

Specific Development of Radionuclide Reporter Genes

[0252] One of the earliest approaches investigated cytosine deaminase as a reporter gene with 5-[3H]-fluorocytosine (5-FC) as the reporter probe (128). Cytosine Deaminase (CD), which is expressed in yeasts and bacteria but not in mammalian cells, converts the antifungal agent 5-fluorocytosine to the highly toxic 5-fluorouracil (5-FU). The 5-FC does not incorporate into mammalian DNA synthesis pathway, however, its by-product 5-FU can block DNA and protein synthesis due to substitution of uracil by 5-FU in RNA and inhibition of thymidilate synthetase by 5-fluorodeoxyuridine monophosphate, resulting in impaired DNA biosynthesis. However, lack of sufficient accumulation of the probe in cytosine deaminase expressing cells (due to efflux of 5-FU) limits its use as an imaging reporter gene (128). More recently a magnetic resonance spectroscopy (MRS) based approach using some modeling has been described using this reporter gene (129). The conversion of ¹⁹F-labeled 5FC to 5FU was followed by MRS in subcutaneous human colorectal carcinoma xenografts in nude mice by using H29 cell lines stably transfected with yeast cd (ycd) gene and a three compartment model was described for non-invasive estimation of ycd transgene expression. The utility of an MRS based approach warrants further investigation.

[0253] One of the most widely used reporter gene systems to image gene expression is the herpes simplex virus type I thymidine kinase gene (HSV1-tk). Thymidine kinases are present in all mammalian cells; they phosphorylate thymidine for incorporation into DNA. Unlike mammalian thymidine kinases, HSV1-TK has relaxed substrate specificity, and is able to phosphorylate acycloguanosine and uracil derivatives which get "trapped" in their phosphorylated state inside the cell. Two main categories of substrates have been investigated as reporter probes for imaging HSV1-tk reporter gene expression: derivatives of uracil [e.g., 2'-fluoro-2'-deoxy-1-β-D-arabinofuranosyl-5-iodo-uracil (FIAU) labeled with radioactive iodine] and derivatives of guanosine [e.g., penciclovir (PCV) radiolabeled with ¹⁸F]. These two major classes of reporter probes share in common the ability to be phosphorylated by HSV1-TK, leading to their accumulation in cell (130). Further details of the HSV1-tk reporter gene approach including a comparison of various tracers, are detailed in a different review article (127). A mutant HSV1-TK enzyme (HSV1sr-39TK) that utilizes ganciclovir (GCV) and penciclovir substrates more

effectively, and thymidine less effectively than the wild-type HSV1-TK enzyme, has been described and successfully applied in PET imaging (131). The HSV1-sr39tk mutant illustrates the ability to engineer the reporter protein and reporter probe to be optimized for each other, leading to a marked gain in imaging signal.

[0254] Another radionuclide reporter gene system uses the dopamine type 2 receptor (D₂R), which binds spiperone {(3-(2[¹⁸F]-fluorethyl)spiperone (FESP))} intra- and extracellularly and thus results in probe accumulation in D₂R expressing cells/tissue (132, 133). The D₂R receptor is a transmembrane protein expressed predominantly in striatum and pituitary and important for mediating the effects of dopamine to control movements. This receptor exerts its response through G-protein mediated signaling cascade involving adenyl cyclase as a second messenger. Spiperone, a D₂R antagonist can be labeled with ¹⁸F to yield radiolabeled FESP and thus has been applied for PET imaging of the D₂R reporter gene (133). Recently, we have investigated the potentiality of two mutant D₂R receptors (D₂R80A and D₂R194A) for PET imaging that can uncouple the downstream cAMP dependent signaling cascade while retaining the property to bind with FESP (134). These two mutants have an advantage of overcoming the undesirable effects of ectopic expression of D₂R receptors on cellular biochemistry by uncoupling signal transduction. The expression of HSV1sr-39tk and D₂R reporter genes can be imaged simultaneously in living mice, with microPET, using two different tracers (e.g., [¹⁸F]FPCV and [¹⁸F]FESP) respectively (**FIG. 19**) (135).

[0255] Somatostatin receptor subtype II (SSTR2) is another reporter gene that has been extensively studied. Nuclear medicine physicians will be familiar with the use of various somatostatin analogues (e.g., radiolabeled octreotide) for imaging tumor cells expressing somatostatin receptor. SSTR2 is normally expressed primarily in the pituitary gland, and also in other tissues like thyroid, pancreas, gastrointestinal tract, kidney, lung etc. When SSTR2 is used as a reporter gene, the receptor can be expressed on the surface of cells that would not normally express this gene, and therefore the use of various tracers can image SSTR2 reporter gene expression. This approach is discussed in further detail in a review article by Rogers et. al. (136). Several other radionuclide based reporter gene approaches have been preliminarily studied and are listed with appropriate references in Table 2.

Gene Therapy Studies

[0256] Precise localization and quantitative assessment of the level of gene expression is highly desirable for the evaluation of gene therapy trials. Most therapeutic transgenes lack appropriate ligands or probes that can be radiolabeled and used to generate images that define the magnitude of therapeutic gene expression. Therefore it is usually necessary to develop and validate "indirect" imaging strategies using a reporter gene in combination with a therapeutic gene. The goal of these approaches is to quantitatively image reporter gene expression and from that infer levels of therapeutic gene expression. Several approaches are currently being developed for indirect imaging of a therapeutic gene and are discussed next.

Fusion Approach

[0257] In recent years, fusion gene/protein technology has become a powerful tool in molecular biology, biochemistry,

and gene therapy. A fusion gene construct contains two or more different genes joined in such a way that their coding sequences are in the same reading frame and thus a single protein with properties of both the original proteins is produced. Examples include HSV1-TK-GFP, (137-139) HSV1-TK-luciferase-Neo (140). An advantage of a fusion approach is that expression of both genes is absolutely coupled. This approach, however, cannot be generalized, as many fusion proteins do not yield functional activity for both the individual proteins or may not localize in an appropriate sub-cellular compartment. Every new therapeutic gene has to be fused to a reporter gene, and often the reporter protein and/or therapeutic protein activity is partially compromised. This approach is therefore not as generalizable as the approaches discussed below.

Bi-Cistronic Approach

[0258] Another approach to express multiple genes from the same vector construct is to insert an internal ribosomal entry sites (IRES) sequence between the two genes. Both the genes are transcribed into a single mRNA from the same promoter but are translated into two different proteins with the help of the IRES sequences. The discovery of cap-independent translation and existence of internal ribosomal entry sites in polioviruses and encephalomyocarditis virus opened a new gateway to construct bicistronic vectors for gene therapy purpose (141-143). IRES sequences are generally 450-800 bp long with complex RNA secondary structures that are required for initiation of translation. Several general translation initiation factors like eIF3, eIF4A, eIF4G and some specific cellular IRES transacting factors (ITAF's) are required to drive proper translation of the second cistron. We recently reported one such bi-cistronic vector where both D₂R and HSV1sr-39tk genes are co-expressed from a common promoter with the aid of EMCV IRES and imaged by microPET in multiple, stably transfected tumors in living mice. (FIG. 20) (144). An approach using β -gal and HSV1-tk was also studied in mice with SPECT (145) Although IRES sequence leads to proper translation of the downstream cistron from a bicistronic vector, expression from the IRES could be cell type specific and the magnitude of expression of the gene placed distal to the IRES is often attenuated (144, 146). This can lead to a lower imaging sensitivity, and methods to improve this approach are currently under investigation. An IRES may also have different behavior in different cell types; a property yet to be fully explored.

Double Promoter Approach

[0259] Two different genes expressed from distinct promoters within a single vector (e.g., pCMV-D₂R-pCMV-HSV1-sr39tk) can potentially be a useful way to couple the expression of two genes. This approach may avoid some of the attenuation and tissue variation problems of an IRES based approach, and is currently under active investigation.

Co-Vector Administration Approach

[0260] Another approach to express both the therapeutic and reporter gene can also be achieved by co-administering both the genes cloned in two different vectors but driven by same type of promoter (147). This approach has recently been tested and shows that the expression of two PET reporter transgenes, HSV1-sr39tk and D₂R, driven by same CMV promoter but cloned in separate adenoviral vectors is

well correlated at the multi-cell (macroscopic) and tissue level when delivered simultaneously. However, it is important to realize that trans effects between promoters on co-administered vectors carrying can potentially affect reporter gene expression.

Bi-Directional Transcriptional Approach

[0261] For many gene therapy applications it would be desirable to not only deliver the therapeutic gene to desired target(s), but to be able to regulate levels of therapeutic gene expression. We have validated an approach in a tumor model in living mice in which a simple antibiotic (doxycycline) can be used in combination with a fusion protein and a bi-directional vector in order to correlatively express two genes of choice (148). This approach leads to bi-directional transcription, two mRNAs, and two proteins. It has the unique feature that the levels of transcription can be regulated by levels of doxycycline. This approach avoids the attenuation and tissue variation problems of an IRES based approach and may prove to be one of the most robust approaches developed to date.

Non-Radionuclide Approaches to Reporter Gene Imaging

[0262] Radionuclide approaches offer a highly sensitive approach for imaging reporter gene expression that can easily be extended from animal studies to human. Nevertheless, other modalities, when used in the appropriate setting, may have desirable characteristics. Magnetic resonance imaging (MRI) techniques recently have obtained encouraging initial results. Using a substrate {(1-(2-(β -galactopyranosyloxy)propyl)-4,7,10-tris(carboxymethyl)1,4,7,10-tetraazacyclododecane)gadolinium(III)-abbreviated as EgadMe} that can be enzymatically processed by β -galactosidase (β -gal) and can generate MRI signal, Louie et al (149) recently demonstrated a MRI based *in vivo* assay of gene expression in living *Xenopus laevis* embryos. After injecting the β -gal mRNA in one of the cells of a two cell stage *X. laevis* embryo, reporter gene expression was followed by introducing EgadMe. The MR images showed high signal intensity in the embryo with both β -gal mRNA and EgadMe in contrast to the embryo with EgadMe alone. Following image correction, it is possible to recognize the eye and branchial arches. The MR image of a live embryo correlates well with images of the same embryo after fixation and staining with X-gal. This approach for routine *in vivo* use is currently limited due to the delivery of the EgadMe substrate which does not have direct cellular uptake. In another study, Weissleder et al described the first non-invasive *in vivo* MR imaging of transgene expression (150). They implanted nude mice with 9 L gliosarcoma cells stably transfected human transferrin receptor (HETR) and control transfected (ETR-) cells followed by injection of iron oxide nanoparticles conjugated with human holo-transferrin (Tf-MION) to image the tumors with MRI. Other MRI/MRS based approaches are reviewed elsewhere (151).

[0263] Optical reporter genes such as firefly luciferase or green fluorescent protein (GFP) are currently being used to monitor gene expression *in vivo* (124, 152). Firefly luciferase gene expression can be imaged using a high sensitivity charged coupled device (CCD) camera. Light is produced through the interaction of luciferase with its substrate luciferin (injected peritoneally) in presence of Magnesium and ATP (152). For the green-fluorescent protein (GFP), an input wavelength must be provided and an output

wavelength of light is produced which can be imaged optically by a fluorescence microscope (153). These optical approaches have the distinct advantage of low background signal, ease of use, and low cost; however, they are limited by light scatter and absorption, limiting studies in deep tissues. Although these optical reporter genes will be extensively used for basic research in small animals, they are not generalizable for human applications. Further examples are referenced in Table 2.

Human Imaging Studies for Gene Therapy

[0264] Studies to image reporter gene expression in human subjects are now beginning. Yaghoubi et. al. (154) reported a study to measure the kinetics, biodistribution, stability, dosimetry and safety of [^{18}F]FHBG in healthy human volunteers, prior to imaging patients undergoing HSV1-tk gene therapy. The study by Yaghoubi et. al. indicated that due to the properties of stability, rapid blood clearance, low background signal, biosafety and acceptable dosimetry [^{18}F]FHBG should be a good reporter probe for HSV1-tk imaging in humans, although [^{18}F]FHBG does not significantly cross the blood-brain-barrier. This may eventually allow not only imaging of gene therapy performed with HSV1-tk, but of any therapeutic gene coupled to HSV1-tk for indirect imaging of the therapeutic gene. In another study, Jacobs et al (155) have shown that [^{124}I]FIAU, another PET reporter probe for HSV1-tk cannot penetrate the blood brain barrier and thus is not a good marker probe for noninvasive localization of HSV1-tk in the central nervous system. However, this probe is useful for areas where the blood brain barrier is disrupted (e.g., glioblastoma). The other reporter genes also have various tracers that have been previously used in human subjects, and therefore can likely be translated to human applications in gene therapy. With the rapid progress in human gene therapy and molecular imaging it is likely that Nuclear Medicine will play a major role in optimizing gene therapy.

Other Applications of Reporter Genes

[0265] Animal applications of the reporter gene imaging assays are particularly important because they allow for the study of many important biological issues in living animals. The use of transgenic animals carrying reporter genes offers unique possibilities for tracking a single animal repeatedly over time during experimental manipulations. Transgenic animals expressing the HSV1-tk gene from tissue specific promoters have been developed to perform cell specific ablation following administration of pharmacologic levels

of pro-drugs such as ganciclovir. A transgenic mouse model in which the HSV1-tk marker/reporter gene is driven by the albumin promoter has been studied (156). The albumin-HSV1-tk transgenic mice have been imaged on a microPET with both [^{18}F]FPCV and [^{18}F]FHBG and clearly demonstrate accumulation of marker/reporter probe in the mouse liver at one hour after injection. Restriction of reporter probe accumulation in the liver is the result of tissue specific transcriptional activation of the HSV1-tk marker/reporter gene by the albumin promoter. The albumin-HSV1-tk mice will be very useful for comparing alternate substrates in vivo and for assessing the reproducibility of assays. Furthermore, these transgenic mice will allow the study of albumin regulation under various manipulations (157). It would be very difficult to develop a tracer specifically targeting albumin, and therefore this indirect approach of imaging albumin gene expression (by imaging HSV1-tk reporter gene expression) illustrates the power of a reporter gene approach to study regulation of an endogenous promoter.

[0266] Other applications of reporter genes include: (1) imaging of cell trafficking by marking specific subsets of cells with a reporter gene ex vivo or through transgenic models. (2) optimization of gene delivery in animal models by studying various vectors carrying a reporter gene. (3) studies of the interaction of tumor cells and the immune system by marking each with a distinct reporter gene. (4) studies of viral infections by marking the virus of interest with a reporter gene. (5) studies of basic cancer biology by monitoring specific gene expression in various tumor models.

Conclusion

[0267] Molecular and functional imaging allows the clinician/researcher to visualize the cellular and/or molecular processes in living tissues. The development of molecular imaging probes is the key to the importance and growth of nuclear medicine. Reporter genes have emerged as a very powerful tool to monitor the delivery, magnitude, and time-variation of therapeutic gene transfer in vivo. The radionuclide based reporter genes like HSV1-tk, D₂R, SS₁Tr2, etc., are currently being used for PET, SPECT and gamma camera imaging. Though still in their infancy, the non-radionuclide based reporter genes are also emerging as another tool for three dimensional, real time, noninvasive imaging of cellular and molecular processes. Nuclear Medicine should help to lead the way for molecular imaging with reporter genes and probes for use with small animal and human imaging.

TABLE 2

Summary of Reporter gene/probe systems				
Reporter gene	Mechanism	Imaging agents	Imaging	References
Cytosine deaminase	Deamination	[^3H]-5-fluorocytosine	Cell Culture study	128
		[^{19}F]-5-fluorocytosine	MRS	129
Herpes-simplex virus type 1 thymidine kinase (HSV1-tk)	Phosphorylation	[^{131}I]FIAU,	SPECT, gamma camera	158
		[^{14}C]FIAU	SPECT, gamma camera	159
		[^{131}I]FIAU	PET	160
		[^{124}I]FIAU	Gamma camera	161
		[^{123}I]IVDU,	Cell Culture	162

TABLE 2-continued

Summary of Reporter gene/probe systems				
Reporter gene	Mechanism	Imaging agents	Imaging	References
Mutant Herpes-simplex virus type 1 thymidine kinase (HSV1-sr39-tk)	Phosphorylation	[¹²⁵ I]IVFRU,	Cell Culture	163
		[¹²⁵ I]IVFAU,		
		[¹²⁵ I]IVAU		
		[¹²⁵ I]FIAU,	Cell Culture	164
		[¹²⁵ I]FIRU		
		[³ H]FFuR	Autoradiography	165, 166, 167
		[¹⁴ C]GCV,		
		[³ H]GCV	PET	167, 168
		[¹⁸ F]GCV		
		[¹⁸ F]PCV	PET	135
Mutant Herpes-simplex virus type 1 thymidine kinase (HSV1-sr39-tk)	Phosphorylation	[¹⁸ F]FHBG	PET	169, 170, 171,
		[¹⁸ F]PCV	Cell culture, PET	172, 173
		[¹⁸ F]FHBG	PET	174, 147
Dopamine2 receptor	Receptor-ligand	[¹⁸ F]FESP	PET	131, 144, 147
Mutant Dopamine2 receptor	Receptor-ligand	[¹⁸ F]FESP	PET	148
Somatostatin receptor	Affinity binding	[¹¹¹ In]DTPA-D-Phe ¹ -octreotide	Gamma camera	133, 144, 147, 148
Oxotechnetate-binding fusion proteins	Binding via transchelation	[⁶⁴ Cu]-TETA-octreotide	Tumor uptake study	175
		[¹⁸⁸ Re]-somatostatin analogue, ^{99m} Tc somatostatin analogue	Gamma camera	176
		[^{99m} Tc] Oxotechnetate	Autoradiography, Gamma camera	177, 136
Gastrin releasing peptide receptor	Affinity binding	[¹²⁵ I]-mIP-Des-Met ¹⁴ -bombesin(7-13)NH ₂ , [¹²⁵ I]bombesin, [^{99m} Tc]-bombesin analogue	Cell culture	178
Sodium/Iodine symporter (NIS)	Active symport	[¹³¹ I]	Cell Culture	179, 180
Tyrosinase	Metal binding to melanin	Synthetic metallomelanins [¹¹¹ In], Fe	Cell Culture	181
Green Fluorescent protein (GFP)	GFP gene expression resulting in fluorescence	Fluorescence	Cell Culture	182
Luciferase (firefly)	Luciferase - luciferin reaction in presence of Mg ²⁺	Bioluminescence	Gamma camera	183, 184
Cathepsin D	Quenched NIRF fluorochromes	Fluorescence activation	Cell culture/MRI	185
β-galactosidase	Hydrolysis of β-glycoside bond	{(1-(2-(b-galactopyranosyloxy)propyl)-4,7,10-tris(carboxymethyl)1,4,7,10-tetraazacyclododecane)gadolinium(III) or EgaMe	fluorescence microscopy	186, 153, 188, 189, 190, 191, 192
Engineered transferrin receptor (TfR)	Receptor-ligand, internalization	Superparamagnetic iron Tf-MION Oxide-tran	Charge coupled device (CCD) camera	152, 193
			CCD camera	194, 195, 196
			MRI	149
			MRI	150

EXAMPLE 5

[0268] The androgen-dependent (AD) phase of prostate cancer requires a functional androgen receptor (AR) and physiological levels of its ligand dihydroxytestosterone (DHT). Prostate cancer eventually transitions to androgen-independent (AI) growth after androgen withdrawal (i.e.,

castration). A major issue is whether AR is functional in AI cancer. We employed gene-expression based molecular imaging and chromatin immunoprecipitation (ChIP) to study AR dynamics during cancer progression in SCID mice bearing human prostate cancer xenografts. A charge-coupled device optical imaging system and an adenovirus-based,

prostate-specific imaging vector were used to visualize the loss of AR activity after castration and restoration of activity upon transition to AI growth. The imaging signal in AI cancer correlated with two benchmarks of AR function in AD cancer: nuclear localization of AR and rising prostate specific antigen (PSA) levels. Chromatin immunoprecipitation (ChIP) data suggest that AR is initially bound to the endogenous PSA enhancer/promoter in AD tumors, releases from the DNA upon castration, but rebinds in the AI state. RNA polymerase II does not dissociate from the PSA gene after castration but its preferred distribution changes from coding regions to the promoter, potentially facilitating the AI transition. Our study demonstrates that AR is functional in and therefore likely to facilitate the AI phase of prostate cancer.

[0269] Prostate cancer growth is initially dependent upon the androgen receptor (AR) (Gelman 2002), a member of the steroid receptor subfamily of nuclear receptors (Freedman 1999). In the presence of its ligand, dihydroxytestosterone (DHT), AR moves from the cytoplasm to nucleus, binds to 15-bp DNA elements (AREs) in enhancers or promoters, and activates expression of genes involved in prostate metabolism. Prostate cancer initially ceases growth with treatments that lower the concentration or effectiveness of DHT. The cancer eventually progresses from this androgen-dependent (AD) state to an androgen-independent (AI) state upon failure of androgen blockade therapies (Abate-Shen and Shen 2000; Feldman and Feldman 2001; Arnold and Isaacs 2002). AR is known to be expressed, and sometimes overexpressed, in many AI cancers (Visakorpi et al. 1995; Gregory et al. 2001) but it has not been shown to be functional. The functionality is an important issue. If AR transcriptional activity is resuscitated in the ligand-deprived environment it would provide a rationale for progression of AI cancer.

[0270] New molecular imaging technologies have made it possible to non-invasively visualize gene activity in real time in living subjects (Contag et al. 2000; Herschman et al. 2000; Contag 2002; Massoud and Gambhir 2003). The development of gene expression- and vector-based imaging approaches permits repetitive and quantitative measurements of gene regulation in a spatial and temporal fashion. These technologies include optical imaging with cooled charge coupled devices (CCD) (O'Connell-Rodwell et al. 2002) and radionuclide approaches such as positron emission tomography (PET) and single photon emission-computed tomography (SPECT) (Gambhir 2002). The pioneering studies in this area originally used potent but constitutive regulatory elements to drive levels of reporter gene expression that could be detected by CCD or radionuclide technologies.

[0271] Our goal was to monitor AR-mediated transcription during the progression of prostate cancer to the AI state in living animals. We employed CCD optical imaging of firefly luciferase because the short half-life of luciferase in conjunction with highly active reporter genes facilitates dynamic measurement of expression occurring over weeks in living animals (Wu et al. 2001a). A major challenge in creating such a system was to generate a robust, prostate-specific, reporter cassette that could detect optical signals in a tumor throughout the course of cancer and respond to changes in AR activity. A second challenge was to correlate the transcriptional activity with benchmarks such as AR

nuclear localization and binding of AR to endogenous promoters. The correlation would ensure that the optical signals were accurately reporting molecular events. We focused our efforts on the prostate specific antigen (PSA) gene because of its AR-responsiveness and prostate specificity (Cleutjens et al. 1996b).

[0272] PSA is a secreted kallikrein protease widely used for evaluating treatment and progression of cancer although it has some drawbacks in prognostic utility (Bok and Small 2002). The PSA promoter and enhancer have been extensively delineated. Both the promoter and enhancer contain AREs necessary for transcriptional activity in AD cancer cell lines like LNCaP (Pang et al. 1995; Cleutjens et al. 1996a; Schuur et al. 1996; Cleutjens et al. 1997a; Cleutjens et al. 1997b; Pang et al. 1997; Zhang et al. 1997). A 440-bp core segment of the enhancer plays the major role in androgen-responsiveness (Cleutjens et al. 1997b). This core segment contains a cluster of AREs, which bind AR cooperatively and contribute synergistically to gene expression (Huang et al. 1999; Reid et al. 2001).

[0273] We previously exploited the synergistic nature of AR action to augment the AR-responsive activity of the PSA enhancer (Wu et al. 2001b). Our effort was designed to track AR activity in cancer via molecular imaging. We re-engineered the PSA regulatory region by duplicating the core portion of the PSA enhancer and by removing non-essential DNA between the enhancer and proximal promoter. This strategy generated a chimeric construct, termed PBC, which maintained low basal expression in non-prostate tissues but enhanced prostate-specific, AR-responsive activity by 20 fold.

[0274] The enhanced activity and specificity of the chimeric constructs were retained in an adenoviral vector expressing firefly luciferase. The adenovector bearing this "first generation" imaging cassette, AdPBC, was able to detect distal metastatic lesions in SCID mouse xenograft models upon intratumoral or systemic injection via tail veins, and visualization with a cooled CCD optical imaging system (Adams et al. 2002). Although the duplicated enhancer provided a significant gain in activity versus the original PSA enhancer, the overall activity was only about 1-5% that of CMV in side-by-side comparisons. This low level of activity made it difficult to dynamically monitor the androgen-response due to the extended time frames required to observe a firefly luciferase signal.

[0275] To further improve the activity we employed a strategy termed two-step transcriptional activation (TSTA). The concept of TSTA was based on an approach originally used to identify enhancers in *drosophila* (Brand and Perrimon 1993). In our TSTA system, the PSA regulatory region was used to express the potent artificial transcription activator GAL4-VP16. GAL4-VP16 acts on a GAL4-responsive firefly luciferase reporter gene, increasing expression well beyond that observed with reporter constructs bearing the PSA regulatory region alone (Iyer et al. 2001). We optimized the system by using GAL4-derivatives containing one, two and four VP16 (VP1, 2 and 4) activation domains, which acted on reporters containing one, two, five and nine GAL4 sites (G1, 2, 5 and 9) (Zhang et al. 2002). Our analysis indicated that the optimal system comprised the augmented PSA enhancer, PBC, driving GAL4-VP2 on a G5 promoter. This approach resulted in robust amplification of expression

in cell culture, while maintaining prostate and ligand response. The optimal system displayed activities significantly higher than the CMV enhancer-driven firefly luciferase (Iyer et al. 2001; Zhang et al. 2002).

[0276] In this paper we incorporated the optimal TSTA system into a replication deficient adenovirus using the simplified recombination system described by Vogelstein and colleagues (He et al. 1998). We chose adenovirus as a vector because it has high infection efficiency and is widely used in gene transfer studies into animals and humans (Pfeifer and Verma 2001). We injected the virus into AD and AI tumors implanted into SCID mice. We demonstrate the ability to image activation, inactivation and reactivation of AR activity during cancer progression. We coupled the imaging with immunohistochemical staining and chromatin immunoprecipitation of AR on the PSA regulatory region in the various stages of tumorigenesis. We generate strong support for the concept that AR is fully active in AI cancer. Our ChIP data also suggest a model whereby the transcription complexes on AR-responsive genes do not disappear in the absence of androgen but remain marginally active and poised to resume full activity in the AI state.

Materials and Methods

Adenovirus Constructs

[0277] AdTSTA was generated from the optimal TSTA plasmid (Zhang et al. 2002). A second NotI site 5' from the PBC enhancer was removed to create unique NotI site in the vector. A SalI-NotI fragment containing the core BCVP2G5-Luc fragment was excised by NotI and partial SalI digestion and inserted into the SalI-NotI site of pShuttle vector (Q-Biogene, Carlsbad, Calif.), which was then incorporated into the adenovirus vector AdEasy™ through homologous recombination. AdCMV was generated as previous described (Adams et al. 2002). The viruses were packaged and propagated in 293A cells (293 cell line stably expressing the E1A gene). The virus was scaled up, purified via a CsCl gradient and titered by plaque assays on 293 monolayers (infectious units=plaque-forming units). Virus is stored at ~1011 pfu/ml in 10 mM Tris-HCl, 1 mM MgCl₂, and 10% glycerol.

Cell Culture and Xenografts

[0278] The human prostate cancer cell line LNCaP was grown in RPMI 1640 supplemented with 10% Fetal Bovine Serum and 1% Penicillin/Streptomycin solution. HeLa, MCF-7, and HepG cells were cultured in DMEM with 10% Fetal Bovine Serum and 1% Penicillin/Streptomycin. Prior to transfection, cells were transferred for 24 hours into medium containing 5% charcoal stripped serum (Omega Sci. Tarzana Calif.). The synthetic androgen Methyltrienolone (R1881; NEN Life Science Products, Boston, Mass.) was added to "ligand positive" samples where indicated.

[0279] Human prostate tumor xenografts were generated on SCID mice as previously described (Klein et al. 1997). Briefly, approximately 1×10⁶ LAPC-9 tumor cells generously provided by Dr. Charles Sawyers were mixed 1:1 with Matrigel (Collaborative Research, Bedford, Mass.) and implanted subcutaneously on the left flank of male SCID (scid/scid) mice. The AI sublines were passaged several rounds in castrated male mice. Single-cell suspension cultures were maintained on PreBM/GM media (Clonetics,

Walkersville Md.). Alternatively, tumors were extracted from founder mice, minced into ~0.2 mm cubes, bathed in matrigel, and implanted subcutaneously onto the left flanks of SCID mice.

Virus Activity Assays

[0280] For luciferase assays, the cultured cells were infected with AdTSTA or AdCMV at an MOI of 0.1. After 48 hours, the cells were harvested and lysed using the passive lysis buffer provided in the firefly luciferase assay kit (Dual-Reporter Luciferase Assay System, Promega, Madison, Wis.). Firefly luciferase activities of 5% of the cell lysates supplemented with 100 µl of D-luciferin were measured using a luminometer (Lumat 9507, Berthod Germany) with an integration time of 10 sec.

Immunoblot Analysis of GAL4-VP16 Expression

[0281] LNCaP cells were grown in 10-cm dishes and infected with AdTSTA at MOI 10. Forty-eight hours later the cells were harvested and lysed with RIPA buffer (10 mM Tris-HCl, 150 mM NaCl, 0.1% SDS, 1% DOC, 1 mM EDTA and 1% NP40). Protein concentrations of the extracts were normalized (Bio-Rad Dc protein assay Kit), the samples were fractionated on 4-15% gradient acrylamide gels (Bio-Rad, Hercules, Calif.) and subjected to immunoblot analysis with rabbit polyclonal antibodies generated against intact GAL4-VP16 or loading control proteins.

CCD Imaging to Detect In Vivo Luciferase Expression

[0282] For the naïve mice, 107 pfu of AdTSTA or AdCMV suspended in 100 µl phosphate buffered saline (PBS) was injected via the tail vein. For the LAPC9 xenografts, a total of 107 pfu of AdTSTA or AdCMV in 40 µl PBS was injected directly into the 0.5-cm diameter tumor xenografts at multiple locations. To ensure adequate distribution throughout the tumor, the injection was carried out twice on two sequential days. The virus was allowed to express the encoded genes and distribute throughout the tissue for 3-4 days prior to imaging. At the days specified in the figures, the mice were anesthetized and injected with ~150 mg/kg D-Luciferin (approximately 3 mg/mouse). Light signals (CCD images) were obtained using a cooled IVIS CCD camera (Xenogen, Alameda, Calif.) and images were analyzed with IGOR-PRO Living Image Software, which generates a pseudoimage with an adjustable color scale. We determined the maximum photons/second of acquisition/cm² pixel/steradian (sr) within a region of interest to be the most consistent measure for comparative analysis. The imaging results correlated closely with luminometry of tissue extracts. Typically our acquisition times ranged from 1 to 10 seconds. These acquisition times were valid in tumors injected only 2 days prior to imaging.

Tumor Immunohistochemical Analysis

[0283] Immunohistochemistry was performed on paraffin-embedded tumor sections with antigen retrieval. Tissue sections were incubated at 4° C. overnight with anti-AR 5 µg/ml (UpState, Charlottesville, Va.). After stringent blocking, washing and incubation with multi-link (BioGenex, San Ramon, Calif.) and alkaline phosphatase label for 20 min at room temperature, sections were washed and developed according to the manufacturer's instructions (BioGenex).

Tumor Chromatin Immunoprecipitation

[0284] Tumors were extracted from the mice and washed with ice cold PBS. The tumors were quickly minced and immersed in 1% formaldehyde solution, where they were further minced and homogenized using a glass dounce. The total incubation in formaldehyde solution was for 30 minutes. Prior to sonication, the cell suspensions were washed 10 minutes each in solution I containing 0.25% Triton, 10 mM EDTA, 1 mM EGTA and 10 mM HEPES, pH 7.5, and in solution II containing 0.2 M NaCl, 1 mM EDTA, 1 mM EGTA and 10 mM HEPES, pH 7.5. Extracts were obtained by 8×15 sec sonication in lysis buffer containing 1% SDS and 10 mM EDTA using a Fisher Scientific Model 550 sonicator at setting 4 with a microtip. Chromatin was purified from insoluble debris by micro-centrifugation at 15,000 rpm for 20 min.

[0285] To perform immunoprecipitation, the chromatin was diluted 1:7 in dilution buffer containing 70 mM HEPES, pH 7.5, 2.5 mM NaCl, 1.5 mM EDTA, 1.5% Triton and 0.6% deoxycholate. The extracts were pre-cleared with pre-immune IgG together with Sepharose A or G agarose beads (Amersham, Piscataway, N.J.) for 1 hour at 4° C. Pre-cleared extracts were incubated with 4 to 6 µg of specific antibodies at 4° C. overnight followed by incubation with 30 µl of agarose A or G beads for 1 hour the next day. The antibodies included the N20 and C19 AR antibodies from Santa Cruz, Biotech; the pol II CTD8WG16 monoclonal from QED Bioscience (San Diego, Calif.); and a TFIIB antibody generated in our lab. The beads were washed twice with buffer containing 50 mM HEPES, pH 7.5, 0.15 M NaCl, 1 mM EDTA, 1% Triton, 0.5% deoxycholate and 0.15% SDS followed by wash with LNDET buffer containing 0.25 M LiCl, 1% NP40, 1% DOC, 1 mM EDTA and 10 mM Tris, pH 8.0. The protein-DNA complexes were then eluted from the beads with 30 to 50 µl elution buffer containing 1% SDS and 1 mM NaHCO₃. The eluates were diluted with TE and incubated at 65° C. overnight to reverse the cross-link. The samples were then treated with proteinase K at 100 ng/µl and RNAase A for 1 h at 55° C. and then extracted with phenol. The DNA was then precipitated with ethanol, resuspended in 30 µl water and subjected to PCR analysis. Typically one 1 cm tumor yielded enough material for 6 PCR reactions. The output sample in the data shown in the ChIP experiments was typically 2% of the DNA added to a ChIP reaction.

[0286] The PCR analyses were performed with four sets of 32P-labeled primers:

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Enhancer:
5'GGTGACCAGAGCAGTCTAGGTG3'
and
5'TGTTTACTGTCAAGGACAATCGAT3'

Promoter:
5'GTATGAAGAATCGGGGATCGT3'
and
5'GCTCATGGAGACTTCATCTAG3'

Middle:
5'TATGCTTGGGGACACCGGAT3'
and
5'TTAGAGCTGGAGTGAAGGATAT3'
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-continued

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Exon
5:5'TAATGGTGTGCTTCAAGGTATCACG3'
and
5'GTGTCCTTGATCCACTTCCGGTAAT3'
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[0287] The PCR cycling protocol was 40 sec at 94° C., 3 minutes at 75° C., 2 minutes at 65° C., followed by 20 cycles of 40 sec at 94° C., 1 minute at 65° C. and 2 minutes at 72° C., followed by a 10 minute extension at 72° C. The PCR products were phenol-extracted, separated on 4% polyacrylamide gels and autoradiographed by exposure to XAR-5 film.

Results

The Adenovector TSTA Imaging System

[0288] FIG. 22 illustrates the adenoviral-based TSTA cassette employed in our study. A modified chimeric PSA promoter containing two copies of the AR-responsive core PSA enhancer is used to drive expression of the fusion protein GAL4-VP2, bearing two copies of the VP16 activation domain. This strategy ensures robust, AR-mediated, prostate-specific expression of GAL4-VP2. In the second step, GAL4-VP2 binds to five GAL4 binding sites positioned upstream of the adenovirus E4 core promoter and activates high levels of firefly luciferase in prostate-derived tissues. Luciferase is measured in cell culture by luminometry and in vivo in D-Luciferin-injected live animals using a cooled CCD optical imaging system (Wu et al. 2001a). The two expression cassettes were joined in a divergently-expressed orientation in the genome of Adenovirus serotype 5, with the E1 and E3 coding regions deleted, which renders the packaged virus replication deficient (He et al. 1998). To validate the ability of this imaging system to accurately detect AR activity we tested its activity, cell specificity and response to androgen in cell culture and then addressed the same criteria in SCID mice with human prostate cancer xenografts. Finally, we correlated the imaging activity with serum PSA levels, AR nuclear localization and binding of AR to the endogenous PSA gene in tumors harvested from the SCID mice.

Prostate Cancer Specificity of AdTSTA

[0289] To assess the expression and androgen responsiveness of the AdTSTA system in cell culture, we infected the model androgen dependent prostate cancer cell line, LNCaP, with AdTSTA (FIG. 23A). Expression of GAL4-VP2, and firefly luciferase were activated significantly in the presence of the synthetic androgen agonist R1881. The largest fold-increase of luciferase activity was observed at the 48-hour time point (FIG. 23A bottom), which correlated with the appearance of GAL4-VP2 by immunoblot analysis (FIG. 23A, top).

[0290] The AdTSTA system maintained cell selectivity in culture (FIG. 23B). An example of these findings is shown for cells derived from prostate cancer (LNCaP), liver (HepG) and cervical cancer (HeLa) (FIG. 23). LNCaP is an androgen-dependent prostate cancer cell line (Horoszewicz et al. 1983), which contains AR and secretes PSA (Tilley et al. 1990; Montgomery et al. 1992). AR expression is not observed in HeLa and HepG. PCR analysis demonstrated that viral infectivity was similar within a two-fold range

among the cell lines we tested. The LNCaP cells displayed significantly higher firefly luciferase activity than HeLa and HepG and responded well to the androgen agonist R1881. MCF-7 cells, an AR expressing breast cancer cell line was also tested but displayed only a low basal level of TSTA expression in the presence of R1881. Thus, the AdTSTA system responds to AR specifically in prostate cells.

[0291] High levels of luciferase are necessary to observe signals from cell-specific promoters. Previous engineering of the PSA enhancer led to the adenovector, AdPBC, which expressed firefly luciferase in a prostate specific manner but with only 5% the activity of CMV. The low level of activity was suitable for initial in vivo studies but two problems limited its utility in evaluating AR function in real time: The extended time frame necessary to observe firefly luciferase expression in tumors and the long acquisition times on the CCD optical imaging system. Side-by-side comparison (**FIG. 23B**) demonstrated that AdTSTA displayed a ligand induced firefly luciferase activity 10-fold greater than AdCMV (**FIG. 23B**) and nearly 200-fold greater than AdPBC. This gain of activity reduced the time frame required to observe a robust CCD signal from a week to two days, and reduced average CCD acquisition times on average from 5 minutes to a few seconds, thereby permitting us to perform the analysis described below.

[0292] The specificity was then evaluated in vivo by tail vein injection into non-tumor bearing SCID mice. **FIG. 24** shows that tail vein injection of AdCMV leads to significant expression in the liver of SCID mice lacking tumors. The figure presents CCD imaging data from a representative mouse at day 14. AdCMV generated a strong liver signal (~106 photons/sec/cm²/sr) on day 6, the signal peaked at day 14 (107 photons/sec/cm²/sr) and then decayed slightly at day 22, when the experiment was terminated. The liver signal was confirmed by imaging the individual organs after sacrifice. In contrast to the data with AdCMV, injection with the same dose of AdTSTA did not result in detectable liver signals in male mice lacking tumors.

[0293] The AdCMV and AdTSTA viruses were then injected intratumorally into mice bearing the LAPC9 xenografts (**FIG. 24B**). LAPC9 is a human prostate cancer derived from a bone metastasis, which was then implanted into SCID mice (Klein et al. 1997). The tumor expresses PSA and wild-type AR. LAPC9 tumors respond to androgen in vivo. Upon castration of male mice, the tumor transiently halts growth and gradually transitions into the AI state. Continued passage of the AI tumors in castrate mice generates a stable AI model, which expresses AR and PSA. We employed an adenovector because of the flexibility it offered, i.e., testing a wide variety of tumors, and because of the difficulty in establishing xenografts that express the TSTA reporter system in a stable manner.

[0294] Direct intratumoral injection of the viruses into LAPC9 AD xenografts followed by CCD imaging demonstrate that the AdTSTA is routinely twice as active as AdCMV in the tumors (**FIG. 24B**). Typically, injection of 10 pfu of AdTSTA generated a robust signal. Therefore, we were able to reduce the amount of virus versus the 109 pfu employed in our previous imaging study with AdPBC (Adams et al. 2002).

[0295] Virus leakage of AdCMV resulted in signals emanating from the liver. The liver signal was confirmed after

sacrifice by imaging the individual organs. In contrast, the specificity of the AdTSTA system, whose tissue distribution parallels that of AdCMV, precluded liver expression.

[0296] We note that the AdTSTA-injected mice did not display a signal in the prostate either by tail vein or intratumoral injection. Under the current conditions we are not achieving substantial delivery to the prostate probably due to virus sequestration in liver and lung (Wood et al. 1999). We did not pursue this issue because our goal was to study AR activity in the xenograft. However, we are currently attempting to discern the specific injection routes and protocols necessary to obtain prostate infection.

AR Signaling is Active in AI Tumors

[0297] To demonstrate the androgen responsiveness of the tumors we first castrated male mice bearing LAPC9 AD tumors and measured serum PSA levels (**FIG. 25**). A decrease or plateau of serum PSA is indicative of successful hormone blockade therapy in humans. The xenograft data revealed that the PSA levels ceased rising and dropped slightly beginning on day 1 and remained flat for many days post-castration, recapitulating the clinical response of androgen blockade therapy. At later time points the PSA began to rise as tumors transitioned from AD to AI, an issue that is discussed further in a later figure.

[0298] Analysis of AD and castrated AD (ADc) tumors revealed that the imaging signal responded well to castration (**FIG. 26**, center panels). The AdTSTA-injected tumors typically emitted >107 photons/sec/cm²/sr on day 4 after virus injection. Castration on day 4 led to a >10-fold drop in the imaging signal by day 10 (**FIG. 26** left panels: AD vs. ADc, $p=0.01$). In contrast, AdTSTA displayed robust activity in established AI mice. Interestingly, the signal actually increased from day 4 to day 10 in AI, whereas no significant increase was observed in AD over the same time frame. These data indicate that the AR-responsive TSTA system is specifically responding to the loss of AR activity in the ADc tumor but that activity is regained in established AI tumors. We will show below that this loss and gain of activity correlates with the drop and rise of PSA in ADc and AI tumors, respectively.

[0299] The imaging activity correlates well with the sub-cellular locale of AR (**FIG. 26** right panels). AR is known to localize predominantly to the nucleus in the presence of androgen. In the absence of androgen, AR becomes more diffuse and localizes to both the cytoplasm and nucleus (Gregory et al. 2001). Immunohistochemical analyses of tumors from the sacrificed LAPC9 animals showed that AR was tightly localized to the nucleus of AD tumors, became diffuse in ADc, but returned primarily to the nucleus in established AI tumors. The staining in ADc was heterogeneous with a small number of cells showing nuclear staining but most showing a diffuse pattern of nuclear and cytoplasmic staining.

[0300] Taken together the imaging and cytology data suggest that AR has resumed functioning in AI cancer. However, numerous other proposals have been made to explain how androgen-responsive genes might function in cells lacking physiological levels of androgen. For example, NF- κ B has been proposed to bind regulatory regions of androgen-responsive genes and might substitute for AR in AI cancer (Chen and Sawyers 2002). However, the predomi-

nant nuclear location of AR in AI tumors suggest AR may be functional. One prediction of this hypothesis is that AR should be bound directly to responsive enhancers and promoters in AI cancer.

Transcription Complex Assembly in Tumors Correlates with the Imaging Signal

[0301] To address our hypothesis we measured AR binding to the endogenous PSA regulatory region using chromatin immunoprecipitation (**FIG. 27**). The PSA enhancer and promoter have been well delineated. Previous chromatin immunoprecipitation experiments performed in cell culture have revealed AR and RNA polymerase II (pol II) binding to the enhancer and promoter in LNCaP cells (Kang et al. 2002; Shang et al. 2002). We confirmed these results in LNCaP cells and then used that knowledge to analyze AR and pol II binding to the PSA gene in the context of AD and AI tumor samples derived from LAPC9 tumors. The tumor ChIP experiments were significantly more difficult to perform than the cell culture ones because the tumor is highly heterogeneous, solid tissue. We rapidly minced and crosslinked the tissue during tumor harvest and performed sonication in detergent containing high levels of SDS followed by ChIP in the presence of low SDS and high levels of deoxycholate.

[0302] We analyzed AR binding to four regions of the gene: The enhancer, the promoter, a region located between the enhancer and promoter, and downstream exon 5 (**FIG. 27**). We predicted that AR would bind only to the enhancer and promoter. **FIG. 27** demonstrates that our procedure worked reasonably well and AR binding was detectable above background to the enhancer and promoter in both the AD and AI samples, although it was more evident in AD in the experiment shown. Each experiment was performed three times and specific signals were confirmed by comparing the AR-antibody signal to the background observed in a mock immunoprecipitation with IgG. The promoter signals were less reproducible than those on the enhancer region (see graph). When normalized to the signal from output DNA in the ChIP reaction, and averaged among experiments performed with different tumors, the binding to the enhancer in AI tumors was only slightly lower than in AD tumors (see graph). In contrast, upon castration (ADc) AR binding to the enhancer and promoter decreased about 4-fold vs. AD tumors. There is still evidence of some specific AR binding in ADc as the signals on the enhancer and promoter are above the IgG background. The residual binding agrees with the cytology data in which some AR remains in the nucleus even in ADc. Furthermore, the PSA levels do not decrease to baseline in ADc but simply drop transiently as the tumor begins to transition to AI.

[0303] To analyze how preinitiation complexes respond to the presence and absence of AR we measured binding of pol II and a representative general factor TFIIB (**FIG. 28**). We predicted that pol II would be distributed among the promoter and downstream exon 5, and that it should disappear upon castration. However, the binding pattern was more complicated. Pol II binding was observed at both the promoter and downstream exon 5 in the AD tumors but its distribution was skewed. A scatter plot of the ratio of pol II signal at exon 5 vs. the proximal promoter shows that in AD tumors the pol II is primarily at exon 5. We interpret the binding to exon 5 as an elongating polymerase. The signal

is specific because it is found only weakly at the enhancer and not in the intervening region. Binding by pol II to the enhancer was previously observed by Brown and colleagues in their LNCaP cell culture study (Shang et al. 2002). The authors interpreted this phenomenon as evidence of DNA looping between the enhancer and proximal promoter. Although we observe binding of pol II to the enhancer, the binding to promoter and exon 5 is stronger

[0304] Remarkably, upon castration, pol II remained bound to the gene. However, as shown by the scatter plot, pol II was localized primarily at the promoter versus exon 5 in four separate experiments. The AI tumors were more complex; different experiments revealed more exon 5 signal and some less. This variation was in contrast to TFIIB, which was present at equal levels at the promoter in AD, ADc and AI in all experiments that we performed. Our interpretation of these findings is that the transcription complex remains intact after androgen deprivation but a greater fraction of pol II is not actively transcribing in ADc vs. AD. This observation correlates well with the drop in the ADc imaging signal measured by CCD and the drop or plateau in serum PSA levels measured by ELISA. The pol II position in AI tumors is more heterogeneous but modestly skewed towards exon 5.

Visualizing the AD-AI Transition in Real Time

[0305] In a human, the failure of androgen deprivation therapy occurs gradually over a period of time that can vary from weeks to years. The LAPC9 models were originally adapted to an androgen-rich environment in immunodeficient mice and then trained to grow in castrate or female mice. We have found that the transition time in animals occurs more rapidly as the tumor grows larger. Typically we begin an experiment when a tumor reaches 0.5 cm but it grows to 1.5 cm within two or three weeks. Usually we have to sacrifice the animals before the transition occurs to adhere to the 1.5-cm tumor size limitation set by our institutional animal care guidelines. However, some individuals transition faster and in these we are able to monitor the transition in real time, as opposed to studying established AI tumors as we described above. The data below illustrate a typical example of an animal that underwent the transition prior to sacrifice (**FIG. 29**).

[0306] In this animal, we injected the AdTSTA virus, imaged the mice four days later, and then castrated the animal when the tumor reached 1 cm. We found that the PSA levels initially dropped 2.4-fold by day 10, six days post-castration, and then began rising again up to day 17, when we had to sacrifice the animal because the tumor had reached the size limit.

[0307] Over this same time frame, the imaging signal was high on day 4 reached a minimum by day 10 and then gradually rose again by day 17 (**FIG. 29**, top). ChIP and immunohistochemical analyses on the tumor from the sacrificed animal revealed that AR had resumed its predominantly nuclear location and was bound primarily to the PSA enhancer, while pol II was found predominantly in the elongating state at exon 5 (**FIG. 29**, bottom). In short, we show an example, where AR has adapted to the androgen-deprived environment and resumed activity in the AI state as measured by imaging, immunohistochemistry and ChIP.

Discussion

[0308] Our study reports the development of a paradigm to study AR dynamics during prostate cancer progression. Cooled-CCD optical imaging is an emerging technology for monitoring transcriptional activity during development, differentiation and disease (Contag et al. 2000; Contag 2002; O'Connell-Rodwell et al. 2002). The ability to employ CCD imaging requires potent reporter systems that can sensitively monitor transcriptional events in living animals. We employed an adenovector-based imaging cassette, which used the TSTA scheme to measure signals that impacted the AR-signaling pathway. The TSTA system is robust and can dynamically monitor a specific androgen response in vivo in the context of a tumor.

[0309] The goal of our study was to determine whether AR was functional in AI cancer. The natural response of an AD tumor to androgen deprivation is transition to an AI state. We found that the AdTSTA imaging system could detect the decreased AR activation caused by removing the systemic source of androgen via castration. We further showed that the signal could be restored in established AI tumors. Finally, we could monitor the loss and gain of androgen responsiveness during a transitory period within an animal. While this transition is significantly more rapid than in a patient, it nevertheless demonstrates the ability of a potent but sensitive imaging system to monitor physiological changes that accompany tumorigenesis.

[0310] The imaging results paralleled several biological and mechanistic benchmarks of AR function. The optical signals paralleled the halt (or decrease) in rising PSA associated with the androgen depletion by castration. We note that castration is unable to completely block progression of well-vascularized prostate xenografts, which ultimately return to the AI state. Also, the correlation was not exact, as the PSA levels decreased on average 2 fold but the imaging signals decreased over 10 fold within the same time frame. We do not yet understand the discrepancy but it may simply reflect the relative half-lives of PSA vs. firefly luciferase. Alternatively, TSTA is an unusually sensitive reporter system designed to respond robustly to androgen. It may be responding more dramatically to changes in the cascade of events that control AR activity. There is a delay in cell culture between the administration of androgen and the appearance of a peak luciferase signal. This delay is due in part to the time required to achieve steady-state activation of the reporter and also to the two step nature of the imaging amplification system. Nevertheless, within the time frames used here, the trends of the imaging and PSA signals were remarkably consistent.

[0311] The imaging signal also correlated somewhat with the cellular distribution of AR, which was nuclear in AD and AI but became diffuse in ADc animals. We note that the levels of AR drop 2-fold in ADc mice but rise again in the AI state. Finally, the optical signal correlated with the AR binding pattern to the endogenous PSA enhancer, which decreased in ADc but increased again in AI cancer. While the cellular localization and enhancer binding of AR clearly cycled, the effects were not absolute. As mentioned above, the PSA levels do not disappear but transiently plateau or drop while the tumors adapt. This could explain the residual AR signals in the ChIP experiments. We do not understand

yet how the tumors adapt and this is the subject of much speculation and research in the field (Grossmann et al. 2001).

[0312] Indeed, one of the key issues in the prostate cancer field is whether recurrent cancer truly employs AR to drive its activity. Our study shows that AR is functional in AI cancer. Although we have only studied the PSA gene we imagine that the resuscitation of AR activity is paralleled on the other genes used by AR in AD cancer growth. Several potential mechanisms that might allow AR function in AI cancer have emerged over the last few years.

[0313] Isolation of the AR gene from tumors and cell lines suggests that certain mutations may permit it to respond to alternate ligands and even antagonists like flutamide (Barack 1996). AR somatic mutations in the Transgenic Adenocarcinoma of Mouse Prostate (TRAMP) model revealed a correlation between reduced androgen dependence and mutations in regions of AR known to interact with co-activators (Han et al. 2001).

[0314] Overexpression of AR has also been observed in AI cancer. For example, analysis of patient samples revealed that the AR gene is amplified in a subset (~30%) of AI tumors (Visakorpi et al. 1995). However, steady state levels of AR are also enhanced in patient samples, cell lines and xenografts even when the gene is not amplified (Gregory et al. 2001; Linja et al. 2001). It has been proposed that the augmented levels of AR or its co-activators can possibly drive AR function with castrate levels of ligand, in part via the principles of mass action. It has also been suggested that AR has adapted to utilize adrenal sources of androgens and possibly convert them to DHT. It is known that castration decreases circulating DHT over 10-fold but smaller effects have been observed when measuring DHT levels within the tumors (Grossmann et al. 2001).

[0315] Mitogen-activated protein kinase (MAPK) may impact AR activity. MAPK, a major signaling pathway involved in cell proliferation, has been linked to AR in numerous studies (Craft and Sawyers 1998; Abate-Shen and Shen 2000; Elo and Visakorpi 2001; Feldman and Feldman 2001; Grossmann et al. 2001; Arnold and Isaacs 2002). Elevated MAPK has been observed in advanced Prostate cancer specimens from patients and in AI xenografts (Gioeli et al. 1999; Mellinghoff et al. 2002). Also, several receptor tyrosine kinases or growth factors, which signal through MAPKs, activate AR-responsive reporter genes in an AI manner when overexpressed in cell culture (Craft and Sawyers 1998; Abate-Shen and Shen 2000; Elo and Visakorpi 2001; Feldman and Feldman 2001; Grossmann et al. 2001; Arnold and Isaacs 2002). We note that the AR in LAPC9 has not undergone mutations but its levels are slightly enhanced in AI tumors and the LAPC9 AI models used here were previously shown to display enhanced MAPK levels (Mellinghoff et al. 2002).

[0316] The relevance of AR in AI cancer is supported by several recent studies. Overexpression of murine AR from the probasin promoter in transgenic mice leads to development of high-grade prostatic intraepithelial neoplasia (PIN), which may be a precursor to prostate cancer (Stanbrough et al. 2001). Conversely, lowering AR levels by injection of a hammerhead ribozyme or antibodies targeted to AR reduces proliferation of AI LNCaP cells in culture (Zegarra-Moro et al. 2002). The effect of AR in AI cell lines apparently

requires DNA binding because the PSA enhancer requires some of its natural AREs to activate reporter genes in AI LNCaP cell lines, although other transcription factors also contribute (Yeung et al. 2000). Our data provide strong direct support for the notion that AR is indeed active and bound to its target enhancers/promoters in natural tumor models of prostate cancer.

[0317] Although our data do not bear on the precise mechanism of AR function in AI cancer they provide evidence that AR is forming transcription complexes. As mentioned above, AR is bound to the PSA enhancer in AD tumors as measured by ChIP. We assume that this binding is paralleled on other AR-responsive genes but this point has not been firmly established. Castration causes much but not all AR to be removed from the PSA enhancer but it apparently rebinds in the AI state. Similarly, pol II is primarily located on exon 5 in AD and in many AI tumors, possibly indicative of an elongating polymerase. The initial loss of DHT by castration causes pol II to relocate mainly to the promoter in ADc. This phenomenon, along with stable TFIIB binding, suggests that the transcription complexes probably remain intact in the absence of androgen, which may facilitate the reactivation of AR-mediated transcription during AI cancer.

[0318] Analysis of other genes such as $\alpha 1$ -AT have also established that pol II can be bound with the GTFs in a quiescent state, prior to binding of activator (Cosma 2002). These data along with older studies of the heat shock locus in *drosophila* (Gilmour and Lis 1986) indicate that a pre-poised pol II may provide a mechanism for maintaining promoter accessibility during a transcriptionally inactive state. AR and pol II are known to cycle on and off the promoter during gene activation in LNCaP cells (Kang et al. 2002; Shang et al. 2002). The peaks of AR and subsequent pol II binding after androgen addition do not coincide suggesting that AR can leave while pol II is engaging the promoter. This phenomenon may be analogous to what is occurring to pol II in ADc tumors.

[0319] The chain of events that lead to the action of pol II at the PSA promoter remain to be firmly established in tumors due to the difficulty of precisely synchronizing cells in living animals. However, we have established an experimental paradigm, where we can screen tumors via gene expression-based imaging followed by detailed molecular analysis (i.e., by ChIP). We have not delved into the precise co-activators driving PSA or tumor progression because the genetic evidence linking specific co-activators to PSA expression is limited. Indeed, we have strong evidence based on RNA interference that at least one co-activator thought to allow AR function has no effect on the endogenous PSA gene. We are therefore systematically probing suspected co-activators by RNA interference to validate their roles in AR-responsiveness.

[0320] On a technical note, we have concerns about GAL4-VP16 and firefly luciferase toxicity. If the toxicity was an issue, we would predict that infected cells would die rapidly and the imaging signal would decay. However, under the conditions employed in our study we are able to obtain relatively persistent imaging signals in tumors within live animals over the course of the experiments, which can last up to a month. Also, the virus is not unusually toxic in cell culture studies, where cells appear to thrive after virus

infection. We note that our ability to employ low doses of virus in the animal studies may permit a less immunogenic response and enable us to transit the system into non-SCID prostate models as well as transgenic animals. We are currently analyzing the TSTA system in lentivirus-transformed lines and in transgenic animals. One limitation of the current study is that the tumor had to be palpable to inject the virus. Lentivirus transformed tumor cell lines are expected to be more stable than adenovirus-infected cells and allow us to measure androgen-responsiveness at the earliest stages of prostate cancer growth. The use of low viral doses could also make possible the application of the system to therapeutic related research for early detection of cancer, a possibility we are currently pursuing.

EXAMPLE 6

[0321] Safe and effective prostate cancer gene therapy requires high magnitude and targeted expression in vivo. Targeted expression has the potential to minimize unwanted side effect of therapy. We improved the activity of native prostate specific antigen (PSA) promoter and enhancer by nearly 20-fold employing a chimeric enhancer manipulation strategy (Gene Ther 2001, 8:1416). Moreover, in vivo application of the prostate specific chimeric viral vector resulted in the specific localization of human prostate metastases in mouse xenograft model (Nat Med 2002, 8: 891). To accomplish efficient in vivo gene transfer we aim to improve the prostate-specific promoter activity to achieve magnitude comparable to strong viral CMV promoter. We employed a two-step transcriptional amplification (TSTA) approach, in which an artificial activator consists of GAL4 and VP16 binds upstream and activates the expression of a therapeutic or reporter gene. The specificity of TSTA is governed by the use of our modified prostate-specific promoter to express GAL4-VP16 activator. We demonstrated that TSTA system exhibits higher activity than CMV promoter but still maintained prostate specificity in cell culture transfections (Mol Ther 2002, 5:223). To optimize this system for in vivo applications, we characterized adenovirus vectors that contains the activator and the reporter component of TSTA in a single or two separate adenoviral vectors. In cell culture infection studies, we confirmed that: 1) both single and separate TSTA system exhibit higher activity than CMV, 2) both maintain androgen regulation, 3) the infection with separate vectors showed higher androgen induction than single vector in prostate cancer cells due to lower basal expression in absence of androgen and 4) high virus to cell ratio leads to diminished cell specificity and androgen regulation. Our TSTA vectors express firefly luciferase gene which can be monitored in living mice by real-time optical CCD imaging. In vivo expression of the single TSTA vector (AdTSTA-FL) exhibits cell selectivity and androgen regulation in prostate cancer xenografts and in murine prostate. Based on these promising results, we are actively investigating this TSTA transcriptionally targeted approach in gene-based therapy and diagnosis for prostate cancer.

EXAMPLE 7

[0322] Gene expression-based imaging should be a powerful tool to assess the real time response of therapy. We have applied non-invasive optical imaging to monitor HSV1 thymidine kinase suicide gene therapy in prostate cancer xenograft models. Here we report the utilization of an

adenovirus-based two-step transcriptional activation (AdTSTA) system to express a potent HSV1 thymidine kinase variant (sr39tk) in the treatment of LAPC-4 prostate tumors. The TSTA system consist of an enhanced PSA promoter driving the expression of a potent synthetic transcriptional activator GAL4-VP16 which in turn activates the expression of the therapeutic gene (sr39tk) or reporter gene (firefly luciferase, FL). For in vivo applications, AdTSTA-FL and AdTSTA-tk were generated to contain the activator and the reporter/therapeutic component in a single vector. The AdTSTA mediated expression is significantly higher than comparable CMV driven vector while maintaining exquisite cell selectivity and androgen regulation. FL-based optical CCD imaging is a sensitive, facile method to sequentially monitor gene expression in living animals. Our strategy is to utilize FL mediated optical signal to measure the relative tk expression in the tumors during suicide therapy. We first demonstrated that co-infection of cells released from LAPC-4 xenografts with equivalent dosage of AdTSTA-FL and AdTSTA-tk produced luciferase activity levels that are correlated with TK protein levels. LAPC-4 tumor bearing mice were divided into 3 therapeutic groups that received intratumoral injection of equal dosage of (i) AdCMV-RL+AdTSTA-FL (control group), (ii) AdCMV-sr39tk+AdCMV-FL (CMV group), or (iii) AdTSTA-sr39tk+AdTSTA-FL (TSTA group). 7 days post viral injection, the animals were given daily intraperitoneal administration of 100 mg/kg ganciclovir (GCV) for five days. Optical imaging just prior to GCV treatment revealed that intratumoral signal in the TSTA group is more than 1 order of magnitude higher than the CMV group. Serial imaging data revealed a more precipitous loss of optical signal in the TSTA group in comparison to the CMV group in a 12 days period after GCV treatment. Detailed histological analysis revealed extensive central tumor necrosis, most dramatic in the TSTA over CMV group, and both treatment groups exhibit much greater cell death than the control group. In this report we demonstrate that TSTA system can mediate highly amplified and tissue-specific gene expression resulting in effective tumor cell killing. Moreover, non-invasive optical CCD imaging is a useful tool to monitor gene expression and therapeutic response.

EXAMPLE 8

[0323] We have previously reported the development of a Two-Step Transcriptional Amplification System (TSTA) to amplify firefly luciferase (fl) reporter gene expression in vivo (Iyer et al, PNAS, 2001). We now report the development and imaging of a novel transgenic mouse line that expresses fl transgene under the control of the Prostate-Specific promoter and VP16 transcriptional activator.

Methods

[0324] The DNA fragment PSEBCVP2-G5-fl used for injection was isolated from the plasmid vector sequence by cutting with appropriate restriction enzymes. Transgenic mice were generated in FVB mice by standard techniques. Seven founder mice carrying the transgene were outcrossed with wild-type animals to yield F1 progeny. Tails from the F1 progeny were clipped at 2 weeks of age and genotyped by PCR. The fl positive mice were imaged at different intervals of time using a cooled Charge Coupled Device (CCD) camera and D-Luciferin as the substrate (3 mg per animal, injected i.p.). The resulting bioluminescent signal was expressed as photons/sec/cm²/steradian (sr).

Results

[0325] In male mice from F1 progeny, the expression of GAL4-VP16 dependent fl gene is observed to be very strong and is primarily restricted to the prostate tissue (5×10^6 p/sec/cm²/sr). In contrast, female transgenic mice show basal levels of fl expression (5×10^4 p/sec/cm²/sr). This suggests the high androgen dependency of the prostate-specific promoter. Additionally, gene expression is also observed in the ears, feet and tail of male mice (1.7×10^6 - 5×10^6 p/sec/cm²/sr). Repetitive imaging over several months demonstrates persistence of the bioluminescent signal. The mice exhibit normal physical characteristics and development and do not show any deleterious effects from the transactivator.

Conclusion

[0326] We have developed a novel transgenic mouse line using the GAL4-VP16 transactivator (driven by a prostate-specific promoter) to amplify the expression of fl reporter gene and shown long-term tissue specific expression of fl. Such transgenic mouse models when coupled with other transgenic lines that spontaneously develop malignancies should play a useful role in the study of early events in cancer progression.

EXAMPLE 9

[0327] The progression of primary prostate cancer requires androgen and a functional Androgen Receptor (AR). Treatments that reduce androgen levels inhibit androgen dependent (AD) cancer progression and AR-responsive gene expression. Ultimately, the cancer regains the capacity for aggressive growth in the androgen-independent (AI) environment and AR-responsive genes are re-activated. A key issue is whether AR is directly mediating this AI response. Through extensive biochemical studies we have identified the key AR responsive elements in the Prostate Specific Antigen (PSA) enhancer. By combining enhancer modifications with two-step transcriptional activation (TSTA) approaches, we have crafted a robust, androgen-responsive optical imaging system targeted to prostate cancer cells. Our "chimeric TSTA" employs a duplicated segment of the PSA enhancer core expressing GAL4 fused to 2 VP16 activation domains. The resulting activators are targeted to reporter templates bearing 5 GAL4 binding sites upstream of firefly luciferase. The entire TSTA imaging cassette is packaged into an Adenovirus for in vivo delivery into SCID mice bearing human prostate cancer xenografts. Using cooled charge-coupled device (CCD) imaging system we observe a robust, tumor-specific luciferase signal that responds to androgen depletion in live AD animal models. Remarkably, we have also observed strong and persistent AR signaling in the AI xenografts. Following the imaging we analyzed the tumors using chromatin immunoprecipitation assays. We identified AR association with the endogenous PSA enhancer and binding of RNA polymerase II, General Transcription Factors (GTF) and the human mediator complexes to the endogenous PSA regulatory regions in both AD and AI tumors. These data combined with immunohistochemical localization studies provide mechanistic evidence that AR is fully functional in AI cancer. We have also exploited the TSTA imaging system to detect cross-talk between the AR-pathway and the MAPK signaling cascade by switching the VP16 activation domain with that of the

MAPK-responsive ELK-1. Using transferrin-enhanced, liposome-assisted gene delivery, we have introduced the AdTSTA-ELK-1 into tumor xenografts through intravenous injection and obtained signals in the distally located tumors. Currently we are assessing the combined MAPK-AR effects in AD and AI xenografts. AdTSTA and AdTSTA-Elk represents a series of tools for in vivo molecular imaging and therapeutic gene targeting in prostate cancer research.

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<210> SEQ ID NO 2
<211> LENGTH: 550
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: firefly
        luciferase (FL) from plasmid vectors PBCVP2G5 (not Sal) and
        PBCVP2G5-L

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<400> SEQUENCE: 2

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Phe	Ile	Gly	Val	Ala	Val	Ala	Pro	Ala	Asn	Asp	Ile	Tyr	Asn	Glu	Arg
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Trp	Leu	His	Ser	Gly	Asp	Ile	Ala	Tyr	Trp	Asp	Glu	Asp	Glu	His	Phe

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Pro Ala Ala Val Val Val Leu Glu His	Gly Lys Thr Met Thr Glu Lys	
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Glu Ile Val Asp Tyr Val Ala Ser Gln	Val Thr Thr Ala Lys Lys Leu	
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Arg Gly Gly Val Val Phe Val Asp	Glu Val Pro Lys Gly Leu Thr Gly	
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Gly Gly Lys Ile Ala Val		
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<210> SEQ ID NO 3
 <211> LENGTH: 286
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence:beta
 lactamase, ampicillin resistance protein from plasmid vectors
 PCBVP2G5 (not Sal) and PCBVP2G5-L

<400> SEQUENCE: 3

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165 170 175	
Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu	
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195 200 205	

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Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
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Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
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<210> SEQ ID NO 4
 <211> LENGTH: 267
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence:Gal4
 DNA-binding domain/V16 transactivation domain
 fusion protein from plasmid vector PCBVP2G5 (not Sal)

<400> SEQUENCE: 4

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
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Glu Gln Leu Phe Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala
 100 105 110

Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser
 115 120 125

Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu
 130 135 140

Thr Val Ser Pro Glu Phe Leu Gln Pro Gly Gly Ser Ala Pro Pro Thr
 145 150 155 160

Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala
 165 170 175

Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
 180 185 190

Asp Gly Asp Ser Pro Gly Pro Arg Ser Ala Pro Pro Thr Asp Val Ser
 195 200 205

Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala His
 210 215 220

Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Asp Gly Asp
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Ser Pro Gly Pro Arg Ser Ser Arg Asn Val Asp Arg Gln Leu Gly Ile
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<210> SEQ ID NO 5
 <211> LENGTH: 8763
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence:PBCVP2G5-L
 plasmid vector comprising effector and reporter sequences
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (300)..(1952)
 <223> OTHER INFORMATION: firefly luciferase (FL) from plasmid vector
 PBCVP2G5-L
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: Complement((3292)..(4152))
 <223> OTHER INFORMATION: beta lactamase, ampicillin resistance protein
 from plasmid vector PCBVP2G5-L
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: Complement((5295)..(6065))
 <223> OTHER INFORMATION: Gal4 DNA-binding domain/V16 transactivation
 domain fusion protein from plasmid vector PCBVP2G5-L
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      35             40             45
Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
      50             55             60
Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
      65             70             75             80
Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
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Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala
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Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser
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Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu
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Thr Val Ser Pro Glu Phe Leu Gln Pro Gly Gly Ser Ala Pro Pro Thr
      145            150            155            160
Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala
      165            170            175
Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
      180            185            190
Asp Gly Asp Ser Pro Gly Pro Arg Ser Ala Pro Pro Thr Asp Val Ser
      195            200            205
Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala His
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Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Asp Gly Asp
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What is claimed is:

1. An expression vector comprising an effector nucleotide sequence, comprising

- a. a modified tissue specific enhancer sequence;
- b. a tissue specific promoter sequence; and
- c. nucleotide sequence encoding a chimeric transactivator operably linked to the modified tissue specific promoter sequence, wherein the encoded transactivator comprises a DNA binding domain and at least one viral transcription activation domain.

2. A vector system comprising the expression vector of claim 1 and a second expression vector comprising a reporter nucleotide sequence, wherein the reporter nucleotide sequence comprises

- a. multiple DNA binding sequences;
- b. an Adenoviral early promoter sequence; and
- c. a first heterologous gene sequence operably linked to the Adenoviral early promoter sequence.

3. The expression vector of claim 1, wherein the effector nucleotide sequence further comprises a second tissue-specific enhancer sequence.

4. The expression vector of claim 1, wherein the modified tissue specific enhancer sequence is from blood, prostate, brain, lung, stomach, bladder, pancreas, colon, breast, ovary, uterus, cervix, liver, muscle, skin, or bone.

5. The expression vector of claim 1, wherein the modified tissue specific enhancer sequence is a modified Prostate Specific Antigen (PSA) enhancer sequence.

6. The expression vector of claim 3, wherein the second tissue specific enhancer sequence is a prostate specific enhancer sequence.

7. The expression vector of claim 1, wherein the DNA binding domain is GAL4 or LexA.

8. The expression vector of claim 1, wherein the viral transcription activation domain is a VP16 or FKHR (fork-head).

9. The expression vector of claim 2, wherein the multiple DNA binding sequences comprise at least 1 and up to 5 DNA binding sequences.

10. The expression vector of claim 2, wherein the multiple DNA binding sequences comprise GAL4, LexA, or PAX3.

11. The expression vector of claim 2, wherein the Adenoviral early promoter sequence is from serotypes selected from a group consisting of Ad 1, 2, 3, 4, and 5.

12. The expression vector of claim 2, wherein the Adenoviral early promoter sequence comprises an E1a, E1b, E2a, E2b, E3, or E4 sequence.

13. The expression vector of claim 2, wherein the Adenoviral early promoter sequence comprises a TATA box sequence.

14. The expression vector of claim 2 further comprising a second heterologous gene sequence operably linked to the first heterologous gene sequence.

15. The vector of claim 1 which is a plasmid, cosmid, or phagemid.

16. The vector system of claim 2 which is a plasmid, cosmid, or phagemid.

17. The vector of claim 1 which is a bacterial vector, yeast vector, adenoviral vector, adenoviral-associated vector, lentiviral vector, or retroviral vector.

18. The vector system of claim 2 which is a bacterial vector, yeast vector, adenoviral vector, adenoviral-associated vector, lentiviral vector, or retroviral vector.

19. A host-vector system, comprising the vector system of claim 2 or 14 and a host cell.

20. The host-vector system of claim 19, wherein the host cell is a prokaryote or eukaryote.

21. A method for expressing a polypeptide encoded by a heterologous gene sequence, comprising growing the host vector system of claim 19 so as to express the polypeptide.

22. A method for expressing a polypeptide encoded by a heterologous gene sequence in a subject, comprising implanting the host vector system of claim 19 in a subject so as to express the polypeptide.

23. A method for detecting expression of a polypeptide encoded by a heterologous gene sequence in a subject, comprising administering the host vector system of claim 19 to a subject under suitable conditions so as to express the polypeptide encoded by the heterologous gene sequence and detecting the polypeptide so expressed.

24. The method of claim 22 or 23 further comprising administering to the subject an agent to induce expression of the polypeptide encoded by the heterologous gene sequence.

25. The method of claim 24, wherein the agent is an androgen.

26. The method of claim 23, wherein the detecting is effected by, positron emission tomography (e.g., PET), single photon emission computed tomography, cooled charged coupled device (CCD) camera optical imaging, magnetic resonance imaging, bioluminescent optical imaging, fluorescence optical imaging, radionuclide imaging, or non-radionuclide imaging.

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